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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 701.41 Seconds
(without alignments)
11157.588 Million cell updates/sec

Title: US-10-051-307-1

Perfect score: 1595

Sequence: 1 gtaatacgaactcactatagg.....tggtaagttggtgtgttc 1595

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1595	100.0	1595	14	US-10-051-307-1 Sequence 1, Appli
2	1482.2	92.9	1598	14	US-10-051-307-2 Sequence 2, Appli
3	1362.4	85.4	1546	14	US-10-051-307-3 Sequence 3, Appli
C 4	293.4	18.4	510	16	US-10-341-961A-371 Sequence 371, App
C 5	195.6	12.3	735	9	US-09-938-842A-2118 Sequence 2118, Ap
C 6	195.6	12.3	735	11	US-09-938-842A-2118 Sequence 2118, Ap
C 7	195.6	12.3	950	9	US-09-770-445-334 Sequence 334, App
C 8	173	10.8	1956	13	US-10-424-599-36321 Sequence 36321, A
C 9	170.4	10.7	875	12	US-10-636-396-4 Sequence 4, Appli
C 10	170.4	10.7	875	17	US-10-636-026-4 Sequence 4, Appli
C 11	167	10.5	909	13	US-10-424-599-103619 Sequence 103619,
C 12	137.4	8.6	717	15	US-10-259-165-389 Sequence 389, App
C 13	137.4	8.6	720	15	US-10-259-165-41 Sequence 41, Appli
C 14	135.2	8.5	1006	17	US-10-437-963-86607 Sequence 86607, A

C 15	132	8.3	1173	13	US-10-424-599-7736 Sequence 7736, Ap
C 16	126.6	7.9	901	13	US-10-424-599-7737 Sequence 7737, Ap
C 17	124.2	7.8	696	15	US-10-259-165-353 Sequence 353, App
C 18	124.2	7.8	699	15	US-10-259-165-109 Sequence 109, App
C 19	124.2	7.8	1052	17	US-10-437-963-89569 Sequence 89569, A
C 20	122.2	7.7	1020	15	US-10-259-165-571 Sequence 571, App
C 21	122.2	7.7	1020	16	US-10-260-238-3136 Sequence 3136, Ap
C 22	120.4	7.5	879	16	US-10-260-238-49 Sequence 49, Appli
C 23	120.2	7.5	922	16	US-10-260-238-4067 Sequence 4067, Ap
C 24	118.8	7.4	805	16	US-10-260-238-4061 Sequence 4061, Ap
C 25	116.8	7.3	911	13	US-10-425-114-27634 Sequence 27634, A
C 26	106.8	6.7	343	9	US-09-770-791-806 Sequence 806, App
C 27	106.2	6.7	808	9	US-09-966-881-46 Sequence 46, Appli
C 28	103.2	6.5	633	15	US-10-259-165-532 Sequence 532, App
C 29	103.2	6.5	633	16	US-10-260-238-1582 Sequence 1582, App
C 30	97.6	6.1	1950	17	US-10-437-963-59877 Sequence 59877, A
C 31	94.2	5.9	3630	17	US-10-437-963-16245 Sequence 16245, A
C 32	90.6	5.7	621	15	US-10-175-389-1 Sequence 1, Appli
C 33	89	5.6	621	15	US-10-175-389-9 Sequence 9, Appli
C 34	88.8	5.6	869	17	US-10-437-963-15621 Sequence 15621, A
C 35	87.2	5.5	1528	13	US-10-425-114-24457 Sequence 24457, A
C 36	84.8	5.3	728	16	US-10-260-238-3135 Sequence 3135, Ap
C 37	81.4	5.1	730	13	US-10-425-114-25389 Sequence 25389, A
C 38	77.2	4.8	935	17	US-10-437-963-82256 Sequence 82256, A
C 39	76.4	4.8	777	15	US-10-259-165-329 Sequence 229, App
C 40	75.8	4.8	695	15	US-10-259-165-630 Sequence 630, App
C 41	75	4.7	826	13	US-10-425-114-23076 Sequence 23076, A
C 42	74.8	4.7	973	17	US-10-437-963-16928 Sequence 16928, A
C 43	71	4.5	3673778	15	US-10-312-841-1 Sequence 1, Appli
C 44	70.4	4.4	529	14	US-10-051-307-6 Sequence 6, Appli
C 45	69.6	4.4	3673778	15	US-10-312-841-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-051-307-1
; Sequence 1, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: SHI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-1

Query Match 100.0%; Score 1595; DB 14; Length 1595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAATACGACTCAGTATAGGCGACGCGGTGTCGACGGCCCTGGCTGATCTTTGTTCA 60
Db 1 GTAATACGACTCAGTATAGGCGACGCGGTGTCGACGGCCCTGGCTGATCTTTGTTCA 60

Qy 61 AAAAAATGAAAAGACGATAGGACCACTGGGTGCAACAATATCTTGCCTC 120
Db 61 AAAAAATGAAAAGACGATAGGACCACTGGGTGCAACAATATCTTGCCTC 120

Qy 121 CAAATCGGTACAGGATGTTACATCTCCCGGTACTTTAAAGTTGACACAGGCGCATTCAC 180
Db 121 CAAATCGGTACAGGATGTTACATCTCCCGGTACTTTAAAGTTGACACAGGCGCATTCAC 180

Applicant

QY 181 CATTATATTTTGGCGTGCATTTGAATTTGTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240
 Db 181 CATTATATTTTGGCGTGCATTTGAATTTGTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240
 QY 241 CGAAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300
 Db 241 CGAAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300
 QY 301 TGAACCTGGTCCAGGCGTACTCGGCTAGGCTGTTTGGTGGTTCGCCGCCACCCGGTGCAC 360
 Db 301 TGAACCTGGTCCAGGCGTACTCGGCTAGGCTGTTTGGTGGTTCGCCGCCACCCGGTGCAC 360
 QY 361 GCAGGACACCAACCAATCACTAGTCATGCAAGAACTCTTACGAGCACCACCAAGTTAC 420
 Db 361 GCAGGACACCAACCAATCACTAGTCATGCAAGAACTCTTACGAGCACCACCAAGTTAC 420
 QY 421 ATCCAGTACGACCCCATATACCTGCTGATGCGGCTAGTGGCCCTAGGCGCATCAATGACCCACA 480
 Db 421 ATCCAGTACGACCCCATATACCTGCTGATGCGGCTAGTGGCCCTAGGCGCATCAATGACCCACA 480
 QY 481 TTTGGCCCCGATCGAAACGTCGGCAGCCGCTTTTCGGGGTCGATGCGGCCCAACGATGTA 540
 Db 481 TTTGGCCCCGATCGAAACGTCGGCAGCCGCTTTTCGGGGTCGATGCGGCCCAACGATGTA 540
 QY 541 TGGACAGTTCTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCACAAAGCAAGAG 600
 Db 541 TGGACAGTTCTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCACAAAGCAAGAG 600
 QY 601 GGAAAGCAAAAGAAAGATCTCAAGTAGCCCATGTTTGGTGAATTTATATGTCGACAAA 660
 Db 601 GGAAAGCAAAAGAAAGATCTCAAGTAGCCCATGTTTGGTGAATTTATATGTCGACAAA 660
 QY 661 TTATTTTGGTACTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAATCG 720
 Db 661 TTATTTTGGTACTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAATCG 720
 QY 721 TATTATAGCAATATCATCTTTGACTAATTAAGAAATATATTAAGAAATATCAATATGATTT 780
 Db 721 TATTATAGCAATATCATCTTTGACTAATTAAGAAATATATTAAGAAATATCAATATGATTT 780
 QY 781 GGTAAAGCTTGAGTGGAAAGATGTAAGAGCGGCTTAATTAATTAATTAATTAATGAT 840
 Db 781 GGTAAAGCTTGAGTGGAAAGATGTAAGAGCGGCTTAATTAATTAATTAATTAATGAT 840
 QY 841 ATAGCCTATAGTACAGTTAACTTTTATTTGGTGATACTTTTGCACATATAAATCTCTGTA 900
 Db 841 ATAGCCTATAGTACAGTTAACTTTTATTTGGTGATACTTTTGCACATATAAATCTCTGTA 900
 QY 901 CGTGACGGAATTTTCTTAAACATAAATATTAAGAAAGCAGCTATTTTCAGATTTTCGTG 960
 Db 901 CGTGACGGAATTTTCTTAAACATAAATATTAAGAAAGCAGCTATTTTCAGATTTTCGTG 960
 QY 961 GCCAAGTTTCTGCATATCTATGCGCCATTTTATCTTTTATCTTTTATCGTCTAGCCTCTA 1020
 Db 961 GCCAAGTTTCTGCATATCTATGCGCCATTTTATCTTTTATCTTTTATCGTCTAGCCTCTA 1020
 QY 1021 GGTACACGTTTGAACATAAATAATCAATAAATTAAGAAAGTAAATTTAGTTTTCCTTTT 1080
 Db 1021 GGTACACGTTTGAACATAAATAATCAATAAATTAAGAAAGTAAATTTAGTTTTCCTTTT 1080
 QY 1081 CATATTAAGTATGAGGATCAATTTTGTAGATCAATCTGAATATCAAAACATCTGATTT 1140
 Db 1081 CATATTAAGTATGAGGATCAATTTTGTAGATCAATCTGAATATCAAAACATCTGATTT 1140
 QY 1141 TAAATACAAACCAATCTGCAAGGGAAGTCTATGATGATGCGTGAAGTGTGTTTGAAT 1200
 Db 1141 TAAATACAAACCAATCTGCAAGGGAAGTCTATGATGATGCGTGAAGTGTGTTTGAAT 1200
 QY 1201 ATTCTTAGTCTAGATGGAGTCAAACTTTTGTAGTCAAAATATCTATTAAGAAAGCCCTTA 1260
 Db 1201 ATTCTTAGTCTAGATGGAGTCAAACTTTTGTAGTCAAAATATCTATTAAGAAAGCCCTTA 1260

RESULT 2

US-10-051-307-2

; Sequence 2, Application US/10051307

; Publication No. US20020170095A1

; GENERAL INFORMATION:

; APPLICANT: DAI, ZIYU

; APPLICANT: SHI, LIPANG

; APPLICANT: HOOKER, BRIAN S.

; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF

; FILE REFERENCE: 059440/0141

; CURRENT APPLICATION NUMBER: US/10/051,307

; PRIOR FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/263,224

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 2

; TYPE: DNA

; ORGANISM: Solanum tuberosum

US-10-051-307-2

Query Match 92.9%; Score 1482.2; DB 14; Length 1598;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 1546; Conservative 0; Mismatches 48; Indels 5; Gaps 3;

QY 1 GTAATACGACTCACTATAGGCGACGCTGGTTCGACGCGCTGGCTGCTATCTTTGTTGA 60

Db 1 GTAATACGACTCACTATAGGCGACGCTGGTTCGACGCGCTGGCTGCTATCTTTGTTGA 60

QY 61 AAAAATTGGAAAAGAAAGCGTAGGACCAATGGAACCTTGGGTGCAACAATATGTTGTCCTC 120

Db 61 AAAAATTGGAAAAGAAAGCGTAGGACCAATGGAACCTTGGGTGCAACAATATGTTGTCCTC 120

QY 121 CAATATGTTACAGGATTTGTATACATCTCCGGTACTTTAAGTTGACCGGCGCATTCAC 180

Db 121 CAATATGTTACAGGATTTGTATACATCTCCGGTACTTTAAGTTGACCGGCGCATTCAC 180

QY 181 CATTATATTTTGGCGTGCATTTGATTTGTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240

Db 181 CATTATATTTTGGCGTGCATTTGATTTGTGGCAATTTCCCTCCACTTTGGATTAGTCGGGG 240

QY 241 CGAAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300

Db 241 CGAAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAATGTCGCAAAATCTAAGTTGT 300

QY 301 TGAACCTGGTCCAGGCGTACTCGGCTAGGCTGTTTGGTGGTTCGCCGCCACCCGGTGCAC 360

Db 301 TGAACCTGGTCCAGGCGTACTCGGCTAGGCTGTTTGGTGGTTCGCCGCCACCCGGTGCAC 360

Applicant

301	TGA	ACTGGTCCAAAGCGGCTACTCGGCTAGGGTGT	TTGGTGGT	TTGGCCCCACCCCGGTGCACT	360	
361	GCAGG	CACACACACCAATCA	CCAGTCA	TGCAGAAACCTCTAC	CAGCACCACTCGAAGTTAC	420
361	GCAGG	CACACACCAATCA	CCAGTCA	TGCAGAAACCTCTAC	CAGCACCACTCGAAGTTAC	420
421	ATCCAGT	TACGACCCCATATACCT	TGCCATCGT	AGTGGCCCTAGGGGCA	TCAATGACCCACA	480
421	ATCCAGT	TACGACCCCATATACCT	TGCCATCGT	AGTGGCCCTAGGGGCA	TCAATGACCCACA	480
481	TTTGGC	CCCCGATCGAAA	CGTCGGCACCGCGT	TTTCGGGGT	CGATCGCCGCCCAACGATGTA	540
481	TTTGGC	CTCGATCGAGACGT	CGGGCACCGCT	TATCGGGT	CGATCGCGCCCAACGATGTA	540
541	TGACAGT	TTGGTTC--	CGTACTCGATAGTGGCAGCAT	TAAGTGA	AAATCAAAAGCAAGA	598
541	TGACAGT	TTGGTTC--	CGTACTCGATAGTGGCAGCAT	TAAGTGA	AAATCAAAAGCAAGA	598
599	AGGGAGAAA	CAAAAAGAGATCT	CAAGTAGCCCAT	GTGTGTG	TGAAATTTATATGTGGACA	658
601	AGGGAGAAA	CAAAAAGAGATCT	CAAGTAGCCCAT	GTGTGTG	TGAAATTTATATGTGGACA	660
659	AATTAT	TTTTTGGTACTTTATATATAGGGA	TATGGCGGCTTT	TGGCACTACGGATATTTAAT		718
661	AATTAT	TTTTTGGTACTTTATATATAGGGA	TATGGCGGCTTT	TGGCACTACGGATATTTAAT		720
719	CGTATTATATAGCA	ATATCATCTTTGAC	TAAATTAATAAGCA	ATAATATTACAAATATGAT		778
721	CGTATTATATACAA	TATCATCTTTGAC	TAAATTAATAAGCA	ATAATATTACAAATATGAT		780
779	TTGGTAAAC	CGTTGAGGTGGAAAAAT	TGATAAGAGCCGCT	TAAATAATTTATTTATGA		838
781	TTGGTAAAC	CGTTGAGGTGGAAAAAT	TGATAAGAGCCGCT	TAAATAATTTATTTATGA		840
839	ATATAGC	TATAGTTACAGTTAACTTTATTTGGTGA	TAACTTTTGACATATAA	ACTCTGT		898
841	ATATAGC	TATAGTTACAGTTAACTTTATTTGGTGA	TAACTTTTGACATATAA	ACTCTGT		900
899	AACGTGACG	GAATTTTCTTAAAACT	AAATATTTAAAAAGCAGCT	ATTTTTCAGATTTTTTCG		958
901	AACGTGACG	GAATTTTCTTAAAACT	AAATATTTAAAAAGCAGCT	ATTTTTCAGATTTTTTCG		960
959	TGGCCAAAG	TTCTTGATACCTTATCTATGCCCAT	TTTTTTACTTTTATCGTT	CTAGCCTTC		1018
961	TGGCCAAAG	TTCTTGATACCTTATCTATGCCCAT	TTTTTTACTTTTATCGTT	CTAGCCTTC		1020
1019	TAGTACAC	GTTTGAAATAAAAATCATAAAAAT	TGAAAGTAAAAAT	TAGTTTTTTTTT		1078
1021	TAGTACAC	GTTTGAAATAAAAATCATAAAAAT	TGAAAGTAAAAAT	TAGTTTTTTTTT		1080
1079	TTCATAT	TACTCGPAGGGATCATTTGTTAGAT	CAATCTGAAATATACAA	ACCATTTCTGAT		1138
1081	TTCATAT	TACTCGPAGGGATCATTTGTTAGAT	CAATCTGAAATATACAA	ACCATTTCTGAT		1140
1139	TTTAAAA	ATCACACCATTTCTGCC--	AAAGGGAGTCTATGTAT	CGGTGACAGAGTGTTT		1196
1141	TTTAAAA	ATCACACCATTTCTGCC--	AAAGGGAGTCTATGTAT	CGGTGACAGAGTGTTT		1199
1197	GATTTAT	CTTTAGTGGATCA	CAACTTTTACTGCAAAATATCTAT	TAAAAAGAAC		1256
1200	GATTTAT	CTTTAGTGGATCA	CAACTTTTACTGCAAAATATCTAT	TAAAAAGAAC		1259
1257	CCATT	TGATGCAATATCTAT	TAAAGAA	CCCCTATTCGTTTATTTTATTTTACGAT		1316
1260	CCATT	TGATGCAATATCTAT	TAAAGAA	CCCCTATTCATTTATTTTATTTTACGAT		1319
1317	CGGAGCA	TGGATATTTTATCTAA	TTAAAAATAAATTTGGAAGGA	ATTGATCGACAAGTCATC		1376
1320	CGGAGCA	TGGATATTTTATCTA	TTAAAAATAAATTTGGAAGGA	ATTGATCGACAAGTCATC		1379
1377	AAGCTT	ATCGTCGATCCACAT	TAAAAATACGTTAGTAT	TGGCTGCTTTTATAGAGAAACAAGT		1436
1380	AAGCTT	ATCGTCGATCCACAT	TAAAAATACGTTAGTAT	TGGCTGCTTTTATAGAGAAACAAGT		1439

RESULT 3

US-10-051-307-3

: Sequence 3. Application US/10051307

Sequence 3, Application US/1995A1
: Publication No. US20020170095A1

; PUBLICATION NO. US20
: GENERAL INFORMATION.; GENERAL INFORMATION:
: APPLICANT: DAT 2TYV

APPLICANT: DAL, ZIU
APPLICANT: SUT I TEANC

APPLICANT: SHI, LIFANG
APPLICANT: HOOKER BRIAN S

APPLICANT: HOOKER, BRIAN S.
TITLE OF INVENTION: GENE PROMOTERS ISOYLATED FROM POTATO AND USE THEREFOR

; TITLE OF INVENTION: GENE

; FILE REFERENCE: 059440/0141

; CURRENT APPLICATION NUMBER: US/11

;
CURRENT FILING DATE: 2002-01-22

.; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 2001-

: NUMBER OF SEQ ID NOS: 14

; NUMBER OF
; SOFTWARE:; SOFTWARE: PAT
; GEO ID NO 3

; SEQ ID NO 3

LENGTH: 1546

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; TYPE: DN
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; ORGANISM: Solanum tuberosum

FEATURE:

NAME/KEY: modified base

LOCATION: (

Query Match 85.4%: Score 1362.4: DB 14: Length 1546:

Query Match 85.1%, Score 1502.4, DB 14, Length 1540,
Best Local Similarity 94.1%, Pred. No. 3 2e-293.

Best Local Similarity 94.1%; Pred. NB. 3.2E-293;
Matches 1460. Concentrative 0. Mismatches 82. Indels 9. Gaps 4.

49 ATCTTTGTTTGAAAAAATTGGAAAAGAACGTAGGACCACATGGACCTTGGGTGCAACAAT 108

QY 49 ATCTTGTTCGAAATAAAATTCGAAATAGTACCTAGGACACATGGACCTTGGGTGCATCAAAI 108

Q. 108. What is the difference between the two types of ... 168

QY 109 ATGTGGTCTCCAAATGTGGTACAAAGATGTACATCTCCGGTACTTAAAGTTGAC 168

120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114

169 CAGGGCA^{TT}CACCA^{TT}TATAT^{TT}GCCG^{TC}GCA^{TT}GAAT^{TT}GTGGCA^{TT}TCCCTCCAC^{TT}G 228

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QY 229 GATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCCGA 288

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QY 289 AATCTAAGTTGTTGAAC TGGTCCAAGGCGTACTCGGCTAGGGTGT TTGGTGGTTTGCCCC 348

349 ACCCGTGCACTGCAGGACACCAACAATCACCGTCATGCACGAACCTCTACCAGCAC 408

QY 409 CATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCTAGCGCAT 468

Db 421 CAAAGACCCAGTGTGGCTCGATCGAGAGCTCGGCCACCGCTATCGGGTGCATGCTG 480
 QY 528 CCCAAACGATGTATGGACAGTGTGGTACCTCGATAGTGGGAGCATAGTGAAGTCA 587
 Db 481 CCCAGACGCTGTATGGACAGTGTGGTACCTCGATAGTGGGAGCATAGTGAAGTCA 540
 QY 588 CAAAGCAAGAGGAGAGAAACAAAGAGAGATCTCAAGTAGGCCATGTTTGGTGAATTT 647
 Db 541 CAAAGCAAGAGGAGAGAAACAAAGAGAGATCTCAAGTAGGCCATGTTTGGTGAATTT 600
 QY 648 ATATGTGGACAAATATTTTGTGACTTTATATATAGGATATGGGCTTTTGGACATA 707
 Db 601 ATATGTGGACAAATATTTTGTGACTTTATATATAGGATATGGGCTTTTGGACATA 660
 QY 708 CGGATATTAATCGTATATATAGCAATATCATCTTTGACTTAATATAACGAAATATAT 767
 Db 661 TGGATATTAATCGTATATATAGCAATATCATCTTTGACTTAATATAACGAAATATAT 720
 QY 768 TACAATATGATTTGGTAAACGTTGAGGTGAAATAATGATAAGAGCGGCTTAATAATTA 827
 Db 721 TACAATATGATTTGGTAAACGTTGAGGTGAAATAATGATAAGAGCGGCTTAATAATTA 780
 QY 828 TTATTTTATGATATAGCTATAGTACAAGTTTAACTTTATTTGGTATGATCTTGCACAT 887
 Db 781 TTATTTTATGATATAGCTATAGTACAAGTTTAACTTTATTTGGTATGATCTTGCACAT 840
 QY 888 ATAACTCTGTAACTGACGGAATTTTCTTAAACCTAAATATAAAGAGCAGCTATTTT 947
 Db 841 ATAACTCTGTAACTGACGGAATTTTCTTAAACCTAAATATAAAGAGCAGCTATTTT 900
 QY 948 CAGATTTTCTGTGCGCAAGTTTCTGCACTATCTATCTATGCCCCATTTTACCTTTATCG 1007
 Db 901 AATATTTTCTGTGCGCAAGTTTCTGCACTATCTATCTATGCCCCATTTTACCTTTATCG 960
 QY 1008 TTCTAGCCTTCTAGTACAGCTTTGAACATAAATAAATAAATAAATAAATAAATAAATA 1067
 Db 961 TTCTAGCCTTCTAGTACAGCTTTGAACATAAATAAATAAATAAATAAATAAATAAATA 1020
 QY 1068 AGTTTTTTTTTCAATATCTAGTGGGATCAATTTGTAGATCAATCTGAATATACAA 1127
 Db 1021 AG---TTTTTTTTTCAATATCTAGTGGGATCAATTTGTAGATCAATCTGAATATACAA 1077
 QY 1128 ACCATCTGATTTTAAATCACAACATCTGCAAGGGAAGCTAT---GTGATCCGT 1184
 Db 1078 ATCATCTGATTTTAAATCATACTATCTGATGATGGAAGCTATGTTGATCTGAT 1137
 QY 1185 GACAAGTGTGATTTATCTTAGTCTGATGATGGAAGCTATGTTGATCTGAT 1244
 Db 1138 GACAAGTGTGATTTATCTTAGTCTGATGATGGAAGCTATGTTGATCTGAT 1197
 QY 1245 ATTAAGAGACCCCTATTTGATGCAATATCTATTAAGAGACCCCTATTTGATCTGAT 1304
 Db 1198 ATTAAGAGACCCCTATTTGATGCAATATCTATTAAGAGACCCCTATTTGATCTGAT 1255
 QY 1305 TATTTTACGATCGGAGCATGATATATTTTACATTAATAAATAAATAAATAAATAAATA 1364
 Db 1256 TATTTTACGATCGGAGCATGATATATTTTACATTAATAAATAAATAAATAAATAAATA 1315
 QY 1365 CGCAAGTCTAAGCTTATCGTTCGATCCACATTAATAAATAAATAAATAAATAAATAAATA 1424
 Db 1316 CGCAAGTCTAAGCTTATCGTTCGATCCACATTTCCCTTAAAGTATGATGCTGCTTT 1375
 QY 1425 AGAAGAACAGTGGATCATCTATAATTTAGTTTAAATAATCTCCCTAATAAATAAATAAATA 1484
 Db 1376 AGAAGAACAGTGGATCATCTATAATTTAGTTTAAATAATCTCCCTAATAAATAAATAAATA 1435
 QY 1485 ATACCTCTAATACTAATATGATCTAACAACAATAAATAAATAAATAAATAAATAAATAAATA 1544
 Db 1436 ATACCTCTAATACTAATATGATCTAACAACAATAAATAAATAAATAAATAAATAAATAAATA 1495
 QY 1545 TTGAGAAATTAATTTGAGGAGCAATATAGTCTATGTTGAGTGGTGGTCTTCTTTC 1595

Db 1496 TTGCAGAAATTAATGGAGCAATAAGTCTATGTTGAAGTTGTTGCTTTC 1546

RESULT 4
 US-10-341-961A-371/c
 ; Sequence 371, Application US/10341961A
 ; Publication No. US20040006787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
 ; APPLICANT: Crasta, Oswald
 ; APPLICANT: Swirsky, Peter
 ; APPLICANT: Mysore, Kiran
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Martin, Gregory
 ; APPLICANT: Ekengren, Sophia
 ; TITLE OF INVENTION: PLANT DEPENDENCE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
 ; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
 ; FILE REFERENCE: BTI.67A2
 ; CURRENT APPLICATION NUMBER: US/10/341.961A
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: 60390249
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: 60261029
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 60348792
 ; PRIOR FILING DATE: 2002-01-14
 ; NUMBER OF SEQ ID NOS: 395
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 371
 ; LENGTH: 510
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 ; US-10-341-961A-371

Query Match 18.4%; Score 293.4; DB 16; Length 510;
 Best Local Similarity 78.5%; Pred. No. 3.3e-55;
 Matches 351; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 49 ATCTTTGTTTGAATAAATTTGAAAAAGACGTAGGACACACATGGACCTTGGGTGCAACAAT 108
 Db 448 ATCTTTGTTTGAATAAATTTGAAAAATTTGACAAATTCAGTAGGACCAATGGACCGTGAATTAACAAT 389
 QY 109 ATTGTTGTCCTCCAAATGTGTGACAAAGATTGTTACATCTCTCGGGTACTTTAAGTTGAC 168
 Db 388 ATTGTTGTCCTCCAAATGTGTGACAAAGATTGTTACATCTCTCGGGTACTTTAAGTTGAC 329
 QY 169 CAGGCAATTCACCAATTTATATTTCCCGTGTCAATTTGATGTTGTCATTTCCCTCCATTG 228
 Db 328 CAGGCAATTCACCGTTTATATTTGGCTGTGCAATTTGAAATTTGATGACATTTTCCAGGGCCAG 269
 QY 229 GATTAGTCGGGGGCAAGATCATCGGTATATTAATCCATCAACTAAAGAAATGTCACCA 288
 Db 268 GCTTAGTTGGGCCCAAGACATAGGGATGTTGAATCCATCAATTAACAGAAATATCCCAA 209
 QY 289 AATCTAAGTTGTTGAACTGTGCTCAAGGCGTACTCGGCTAGGGTGTGTTGGTGGTGGCC 348
 Db 208 AATCTAAGTTTACCAAACTGGTTTCAAGCGTATTTCAGCTAAGTTGTTGGTGGTGGCC 149
 QY 349 ACCCGTGTGATCGAGGACACCAACCAATCAACAGTCAATGACGACCTTACCAGCAC 408
 Db 148 ATCTTTTGAATCAGGACCTCCACCAATCACCAGTCTGGCACAACCTCTTCCAGCAC 89
 QY 409 CATGGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTCCCTAGTCCCTAGGCGCAT 468
 Db 88 CATCAAGTTGCAATTTAGTACGACCCCAATACGTGCCATTTTAGTGCAGGTGGGCCCC 29
 QY 469 CAATGACCAACATTTGGCCCGGATCGA 495
 Db 28 AAAACCCACCACTCTGACCTCTCTCGA 2

RESULT 5

```

US-09-938-842A-2118/c
; Sequence 2118, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match      12.3%; Score 195.6; DB 9; Length 735;
Best Local Similarity 62.3%; Pred. No. 2.6e-33;
Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

Qy 46 GGTATCTTTGTTGAAAAAATGGAAAGAACGTAGGACCAATG-----GACCTTTGGG 99
Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATGATCCCTGACCGTTGC 527

Qy 100 TGCACAAATATTGTTGCTCTCCAAATGTGTTCAAGAGTATTGTTACATCTCCGGGTACTT 159
Db 526 TACAACAGTATTGGTTGCTGCTGAATACAGTACAGGTTGTTGATCCACCTGGGGCTC 467

Qy 160 TAAGTTGACAGGCAATTCACATTTATATTGCGGTGCAATGAAATGTTGGCATTTCC 219
Db 466 TCAACAGTTTGGACATTTGCTGTTTATGCTGCGGTACATAGTATCGATGGCAGTTC- 408

Qy 220 CTCACATTGATAGTGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAA 279
Db 407 -----GAACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA 356

Qy 280 TGTCCAGAAATCTAAGTTGTTGAATGTTGCTCAAGCGCTACTCGGTAGGGTGTGGTG 339
Db 355 TATCGTAGAAGTCTAAGTTGTTGAATGTTGCTCAAGCGTACTCAGCAACGTGTTGGTG 296

Qy 340 GTTTGCCCCACCGGTGCACTGCAGGACACCAACCAATCAACAGTCAATGCAAGACCTC 399
Db 295 GCTGTCCCGCCAGCAGTACATTTGGAGTCCACACTGCAGTCAACAGTTTGGCATCGGCCAC 236

Qy 400 TACAGCACCATTGAGTTTACATCCAGTACAGCCCATATCTGCTGCTAGTGTGCCCC 459
Db 235 GACCTGAGAGTCAAAAGTTACAAATGGTCTACCCCAATCGTGCCATTTAGTGCCCC 176

Qy 460 TAGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTGCGCACCCCGTTTCGGGGT 519
Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCG--CCACCTCCAGGGCT 118

Qy 520 CGATGCCGCCCAACAGTATGAGACAGTTGTTGCTACCTCGATAGTGGCAGCATAGT 579
Db 117 TGCGGACGCCACACGGTAACTACATTTGGTATTGAGATTTGGAATTTGGCGGCTGTTGC 58

Qy 580 GAAAGTCAAAAAGCAAGGAGGAGAGAAACAAAAGAGATCTCAAG 625
Db 57 GGTGAGATGAGCAAAAGTGCGGAAATATGAAAGTAGAGACCAAG 12

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RESULT 6
US-09-938-842A-2118/c

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; Sequence 2118, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match      12.3%; Score 195.6; DB 11; Length 735;
Best Local Similarity 62.3%; Pred. No. 2.6e-33;
Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

Qy 46 GGTATCTTTGTTGAAAAAATGGAAAGAACGTAGGACCAATG-----GACCTTTGGG 99
Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTGC 527

Qy 100 TGCACAAATATTGTTGCTCTCCAAATGTGTTCAAGAGTATTGTTACATCTCCGGGTACTT 159
Db 526 TACAACAGTATTGGTTGCTGCTGAATACAGTACAGGTTGTTGATCCACCTGGGGCTC 467

Qy 160 TAAGTTGACAGGCAATTCACATTTATATTGCGGTGCAATGAAATGTTGGCATTTCC 219
Db 466 TCAACAGTTTGGACATTTGCTGTTTATGCTGCGGTACATAGTATCGATGGCAGTTC- 408

Qy 220 CTCACATTGATAGTGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAA 279
Db 407 -----GAACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA 356

Qy 280 TGTCCAGAAATCTAAGTTGTTGAATGTTGCTCAAGCGCTACTCGGTAGGGTGTGGTG 339
Db 355 TATCGTAGAAGTCTAAGTTGTTGAATGTTGCTCAAGCGTACTCAGCAACGTGTTGGTG 296

Qy 340 GTTTGCCCCACCGGTGCACTGCAGGACACCAACCAATCAACAGTCAATGCAAGACCTC 399
Db 295 GCTGTCCCGCCAGCAGTACATTTGGAGTCCACACTGCAGTCAACAGTTTGGCATCGGCCAC 236

Qy 400 TACAGCACCATTGAGTTTACATCCAGTACAGCCCATATCTGCTGCTAGTGTGCCCC 459
Db 235 GACCTGAGAGTCAAAAGTTACAAATGGTCTACCCCAATCGTGCCATTTAGTGCCCC 176

Qy 460 TAGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTGCGCACCCCGTTTCGGGGT 519
Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCG--CCACCTCCAGGGCT 118

Qy 520 CGATGCCGCCCAACAGTATGAGACAGTTGTTGCTACCTCGATAGTGGCAGCATAGT 579
Db 117 TGCGGACGCCACACGGTAACTACATTTGGTATTGAGATTTGGAATTTGGCGGCTGTTGC 58

Qy 580 GAAAGTCAAAAAGCAAGGAGGAGAGAAACAAAAGAGATCTCAAG 625
Db 57 GGTGAGATGAGCAAAAGTGCGGAAATATGAAAGTAGAGACCAAG 12

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RESULT 7
US-09-770-445-334/c
; Sequence 334, Application US/09770445

```
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Oiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Pries, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hufban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-334

Query Match      12.3%; Score 195.6; DB 9; Length 950;
Best Local Similarity 62.3%; Pred. No. 3e-33;
Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

QY 46 GGTATCTTTGTTGAAAGAAATCTTGAGTACTGATCGGTACATGATCCCTGACCCGCTCG 535
DB 594 GGCATCTCTGTTAAAGAAATCTTGAGTACTGATCGGTACATGATCCCTGACCCGCTCG 535
QY 100 TGCAACAATATTTGTTGTCCTCAAAATGCTGTAACAAGATTTTACATCTCCGGGTACTT 159
DB 534 TACAAAGATATTTGTTGTCCTCAAAATGCTGTAACAAGATTTTACATCTCCGGGTACTT 159
QY 160 TAAGTTGACAGGCAATTCACATTTATATTTCCGGTGCATTTGAATTTGTTGCAATTTCC 219
DB 474 TCAACAGTTTGGACATTTGTCCTGTTTATGTCCTGGGTACATAGTATCCGATGGCAGTTC- 416
QY 220 CTCACATTTGATTTAGTTCGGGCGAAGTCTATCGGTATATTAATCCATCAACTAAAGAA 279
DB 415 -----GAACTAGTTGGGCTAAATCCATAGTATTTAAATCCATCAACTAAAGAA 279
QY 280 TGTCGCCAGAAATCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGTTGTTGGTG 339
DB 363 TATCGTAGAAGTCTAAGTTGTTGAACTGTTCCAAAGGCTACTCGGTAGGTTGTTGGTG 304
QY 340 GTTTGCCACCCCGGTGCACTGCAGACACCAACCAATCAACAGTCTGCAAGAACCTC 399
DB 303 GCTGTGCCCCAGCAGTACATTTGAGTTCACCACTGCACTGCACTGCACTGCACTGCACT 244
QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATCTCTGCACTGTTAGTCCGCC 459
DB 243 GACCTGAGAGTCAAGTTACATTTGTTCTACCCCAATCCGTGCACTTTAGTCCGCC 184
QY 460 TAGCGCATCAATGACCAATTTGGCCCGCATTCGAAAGCTGCGGCAACCCGCTTTGGGGT 519
DB 183 CCGCGCATCTAGCTCCATGATTTGGCCGAGCATCTAGAGCTCGG--CCACCTCCAGGGCT 126
QY 520 CGATGCCGCCCAACAGATGATGACAGATTTGTTGCGTACCTCGATAGTGGCAGCATAGT 579

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36321
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1956)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_WRT3847_132800C.1
US-10-424-599-36321

Query Match      10.8%; Score 173; DB 13; Length 1956;
Best Local Similarity 59.5%; Pred. No. 4.9e-28;
Matches 355; Conservative 0; Mismatches 225; Indels 17; Gaps 3;

QY 45 TGGTATCTTTGTTGAAAGAAATTCGAAAGAACCTAGGACCA------TGGACCTTGG 98
DB 1338 TGGCACCTATCTTTGAAGAACCTTTGAGTAGTTTGTGGGCCACACAGCTTCTTGGCCATTG 1279
QY 99 GTGCAACAATATTTGTTGCTCCAAATGTGTCAAGATTTTACATCTCCGGGTACT 158
DB 1278 GTGAGCAATATCTATCTGCTTTAAACACAGTGCAGGGTTTGTGATCCCCAGGTGCC 1219
QY 159 TTAAGTTGACACAGGCAATTCACATTTATATTTTCCGTGCAATTTGTTGTTGCAATTC 218
DB 1218 CTTAATGCGCCCGGCACTGCCCCATTTGATATCAGCGCTGCAACTGATTTTGTGACACCCA 1159
QY 219 CCTCCACTTGGATTAGTCGGGCGAAGTGCATCGGTATATTAATCCATCAACTAAAGAA 278
DB 1158 CC-----GTTTGAAGGTAGAGTCCATCGGAATTTGAACCCGTCCACAAAGAG 1108
QY 279 ATGTCCCAGAAATCTAAGTTTGTGAAGTGTCCAAAGGCTACTCGGTAGGTTTGGT 338
DB 1107 ATGTGCTAGAAATCTGTTGCCAAATTTGTTTCAACGCAATTCGCAAGTGTGTTGGGA 1048
QY 339 GGTTCGCCACCCGTTGCACTGCAGGACACCAACCAATCAACAGTCTGCAAGAACCT 398
DB 1047 GGGACCCCGGAGCTTGGCAATTTAGGCGCGCCGCTGTCAGTCTCCCGTTTGGCAGCGGCG 988
QY 399 CTACAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATCTGCACTGTTAGTCC 458
DB 987 CGGCGGTGCAATCAAGTTTGCACCCCGTGGGCCCATATACGGGCAATGCGAGTGC 928
QY 459 CTAGCGCATCAATGACCAATTTGGCCCGCATTCGAAAGCTGCGGACCCGCTTCCGGG 518
DB 927 GGGTTACCCAGAGGTTCCACGTTTGGCCACGCTGCGGTCAGACCGCGGCTCCAC--CGGAC 870
QY 519 TCGATGCGGCCCAACGATGATGACAGTGTGCGTACCTCGATAGTGGCAGCATAG 578
```

Db 869 TCGCGCGGCCACACCGTGTAGGGCAATTGTTGACATCTCGAAGTTTGCAGCATGTA 810
 Qy 579 TGAAGTGTCAAAAAGCAAGAGGAGAGAAACAAAGAAAGATCTCAAGTAGCCCATGT 635
 Db 809 TTGTTGCCAAAGGTAAGGCCAACGTTTAGCAGAGACACAGTGCCCAAGTAAACCATTT 753

RESULT 9

US-10-636-396-4/c
 ; Sequence 4, Application US/10636396
 ; Publication No. US20040073971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duvick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,396
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 ; US-10-636-396-4

Query Match 10.7%; Score 170.4; DB 12; Length 875;
 Best Local Similarity 59.7%; Pred. No. 1.2e-27;
 Matches 325; Conservative 0; Mismatches 211; Indels 8; Gaps 2;
 Qy 49 ATCTTTGTTTGAAGAAATGGAAGACGCTAGGACACATGACCTTGGGTGCAACAAT 108
 Db 577 ATCTGCTTGAAGAAACCTTGATTAATCAGTTGTCACATTTCCAGAGTTGCAACAAT 518
 Qy 109 ATTGTTGTCCTCCAAATGTGTACAGGATTTTACATCTCCGGTACTTTAAGTTGAC 168
 Db 517 ACTGATCAGTTTGTACACGGTGCAAGGTTATTGCACCCGCGCAGGACCGTAACTCAC 458
 Qy 169 CAGGCAATCACCATTATTTGCGTGCAATGAATGTGTGCAATTTCCCTCCACTTG 228
 Db 457 CAGGACACTGGCCATTGATATCCGACGTACATGAGATACCCCGGTGCACCC-----AT 404
 Qy 229 GATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 288
 Db 403 TAGAATGGGTCTAAACACCATCGGCACATTTGAATCCGTCACAGAGAAATGTCAAGA 344
 Qy 289 AATCTAAGTTGTGAATCGTCAAGCGTACTCGGCTAGGGTGTGTTGGTGGTTGCCCC 348
 Db 343 AATCAAGATTGTGAATCGTCTCAAGCGTACTCGGCCAATGTGTGGGTGGGTACCAT 284
 Qy 349 ACCCGGTGCACTGCAGGACACACCAATCACCAGTCATGCAACCACTTACCAGCAC 408
 Db 283 AGTTTGGCATTTGGAGAGACCGTTGCAATCACCAGTCTGACACCTGCTCGCCAGAAC 224
 Qy 409 CATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTGTGCCCCCTAGCGCAT 468
 Db 223 CATCAAGTTGCAATTTGTTTGGGGGCATATACGGGCTCCTGCTGCGCAGTCCGACGG 164
 Qy 469 CAATGACCCCATTTGGGCCCCGATCGAAGCGTCCGACCCGCTTTCGGGGTCGATCGGC 528
 Db 163 TTAAGACACCGTTTGGCTGAGTTAAGTTGTGCGCGCCAC--CAGGCACCGCACCAGC 106
 Qy 529 CCAACGATGTGACAGATTGTTGCGTACCTCGATAGTGGCAGCATAAAGTGAAGTCACT 588

Db 105 CCARACGGTGTATGACAGTGTTCGATAGTAGTGAACACGGCTGCATTGTATAGTAAA 46
 Qy 589 AAAA 592
 Db 45 AAGA 42

RESULT 10

US-10-636-026-4/c
 ; Sequence 4, Application US/10636026
 ; Publication No. US2004011761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duvick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,026
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 ; US-10-636-026-4

Query Match 10.7%; Score 170.4; DB 17; Length 875;
 Best Local Similarity 59.7%; Pred. No. 1.2e-27;
 Matches 325; Conservative 0; Mismatches 211; Indels 8; Gaps 2;
 Qy 49 ATCTTTGTTTGAAGAAATGGAAGACGCTAGGACACATGACCTTGGGTGCAACAAT 108
 Db 577 ATCTGCTTGAAGAAACCTTGATTAATCAGTTGTCACATTTCCAGAGTTGCAACAAT 518
 Qy 109 ATTGTTGTCCTCCAAATGTGTACAGGATTTTACATCTCCGGTACTTTAAGTTGAC 168
 Db 517 ACTGATCAGTTTGTACACGGTGCAAGGTTATTGCACCCGCGCAGGACCGTAACTCAC 458
 Qy 169 CAGGCAATCACCATTATTTGCGTGCAATGAATGTGTGCAATTTCCCTCCACTTG 228
 Db 457 CAGGACACTGGCCATTGATATCCGACGTACATGAGATACCCCGGTGCACCC-----AT 404
 Qy 229 GATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 288
 Db 403 TAGAATGGGTCTAAACACCATCGGCACATTTGAATCCGTCACAGAGAAATGTCAAGA 344
 Qy 289 AATCTAAGTTGTGAATCGTCAAGCGTACTCGGCTAGGGTGTGTTGGTGGTTGCCCC 348
 Db 343 AATCAAGATTGTGAATCGTCTCAAGCGTACTCGGCCAATGTGTGGGTGGGTACCAT 284
 Qy 349 ACCCGGTGCACTGCAGGACACACCAATCACCAGTCATGCAACCACTTACCAGCAC 408
 Db 283 AGTTTGGCATTTGGAGAGACCGTTGCAATCACCAGTCTGACACCTGCTCGCCAGAAC 224
 Qy 409 CATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTGTGCCCCCTAGCGCAT 468
 Db 223 CATCAAGTTGCAATTTGTTTGGGGGCATATACGGGCTCCTGCTGCGCAGTCCGACGG 164
 Qy 469 CAATGACCCCATTTGGGCCCCGATCGAAGCGTCCGACCCGCTTTCGGGGTCGATCGGC 528
 Db 163 TTAAGACACCGTTTGGCTGAGTTAAGTTGTGCGCGCCAC--CAGGCACCGCACCAGC 106

QY 529 CCAACGATGATGACAGATTGTCGTACCTCGATAGTGCAGCATAAGTGAAAGTCAC 588
Db |||||
QY 105 CCAACGGTGTATGACAGATTGTTTCGAATAGTGAACACGGCTGCATTGGTATAGTGAAA 46
Db |||||
QY 589 AAAA 592
Db |||||
45 AAGA 42

RESULT 11

US-10-424-599-103619/c
; Sequence 103619, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hui-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: SOY NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103619:
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
US-10-424-599-103619

Query Match 10.5%; Score 167; DB 13; Length 909;
Best Local Similarity 60.7%; Pred. No. 6.9e-27;
Matches 327; Conservative 0; Mismatches 205; Indels 7; Gaps 3;

QY 46 GGTATCTTTGTTGAAATAATTGAAAGAACGTAGGACACATGGACCTTGGGTGCAAC 105
Db |||||
QY 631 GGCACCTTTGCTGAGAAATCTGGAATATCATGTGGGCCACAGCTACCGAATTCAC 572
Db |||||
QY 106 AATATTGTTGCTCCAAATGTGTTACAGAGTTGTACATCTCCGGGTACTTTAAGTT 165
Db |||||
QY 571 AGTACTGGTCGGTTTTGAAGACAGTGAAGGTTGTGCAACCTCTTGAATCTTTAGCT 512
QY 166 GACAGGGCATTCACCATTTATTTTCCGTCGATGAAATGTGTGGCATTTTCCCTCCAC 225
Db |||||
QY 511 CACTAGGGCACTGTCCGTTAATGTCCGACGTGCA---GCTTATGCCACGTGTGCATCCAT 455
QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCCC 285
Db |||||
QY 454 TCG---AGGTTGACATAAGTCCATGGCACGTTAAACCGTCGACGAGGAGATGCGA 398
QY 286 AGAAATCTAAGTTGTAATCTGTCAGCGCTACTCGGCTAGGCTGTTTGGTGTTC 345
Db |||||
QY 397 AGAAGTCCAAATTTGTAACCCGTTTCCGCGCTATTTCAGCAGGGTGTGTTGGAGGCGCAC 338
QY 346 CCCACCCGGTGCATGCGAGGACACCAACAAATCACCAGTCATGACGAACTCTACACAG 405
Db |||||
QY 337 CGTAAGCTTTGCAATCGAGGACACCCCGCGAGTCACCGGTCTGGCATCCACCGGCGCG 278
QY 406 CACATCGAAGTTACATCCAGTACGACCCCATATATCTGCGCATCTGTAGTGCCTTAGGG 465
Db |||||
QY 277 AACCGTTCGAAGTTGACGCGGTTTCCGGGCCCAACCGGGGCCCTTTTCGTTCTTCGAGGCA 218
QY 466 CATCAATGACCCACATTTTGGCCCGGATCGAAACGTGCGCACCGCTTTCGGGGTC-GATG 524
Db |||||
QY 217 CGTCCACGACCAATGACTGGCCCGGTTTAAATGACGACCAACCGCCAAACGAGGACAGC 158
QY 525 CCGCCCAACAGATGTATGGACAGTTGTGCGTACCTCGATAGTGGCAGCATAGTGAAA 583
Db |||||
QY 157 CAGCCACAGACAGTGTATGTGCATCGGTTTGTGATTTTCAAAACCTTGCAGCATATGCGAA 99

RESULT 12

US-10-259-165-389/c
; Sequence 389, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hui-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 389
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-389

Query Match 8.6%; Score 137.4; DB 15; Length 717;
Best Local Similarity 56.9%; Pred. No. 2.4e-20;
Matches 292; Conservative 0; Mismatches 216; Indels 5; Gaps 2;

QY 98 GGTGCAACAAATATTGTTGCTCTCCAAATGTGGTAAAGGATTTGTACATCTCCGGGTAC 157
Db |||||
QY 541 GGTGACAGTACTGTTCTCTTTGAACACCGTGCACGCGTGTTCACCGCGCGCGCGC 482
QY 158 TTTAAGTTGACACGGGCAATTCACATTTATTTTGGCGTCGATGAATTGTG---TGSC 213
Db |||||
QY 481 CCTAGCTCGCTCGGCGCACTGCCCCCGCACGTCGCGCTCGCACCGCGCGCGCCCTTGGC 422
QY 214 ATTTCCCTCCACTTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTA 273
Db |||||
QY 421 GCACCGCGCGCTCGCGCGGGGAGGAAGTCCATGGGCACGTTGAATCCGTCGATGA 362
QY 274 AAGAAATGTCACAAATCTAAGTTGTGAAGTGTGAACTGGTCCAAAGGCGTACTCGCTAGG 333
Db |||||
QY 361 GGGAGATGTGGAAGAAGTCGAGGTTGCTGAAGTGTGCTGAGTGTTCAGCGGCACTCCGCG 302
QY 334 TTGTTGTTTTCGCCCACTCGGTGACATGTCAGGACACCAACCAATCACCAGTATGACAG 393
Db |||||
QY 301 TGGGGGCTGCGCGTACGCGCGCACCGCGAGCGCGCGCGCTCGCGCTCTGAGACC 242
QY 394 AACCTCTACAGCAACATCGAAAGTTACATCCAGTACGACCCCATATACCTGCCCATCTAG 453
Db |||||
QY 241 GCGCGTTGCGCTGCGCGTTCGAAGCTGACGCGCGTGCAGCGCGCGCACACGCGCGCGCTCG 182
QY 454 TGCCCTTAGGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTCGACACCGC-CTT 512
Db |||||
QY 181 TGCGGGCGGACGTCGATCACCACCTGCTGCCCGGCTCCAGTGTGCTGCTGCCCGCGCG 122
QY 513 TCGGGGTGATGCGCGCCCAAAACGATGTATGGAAGTGTGTTTCGTAAGTGTGCGTACTCGATAGTGGCAG 572
Db |||||
QY 121 ACGGACAGGCTGCGCGCCACACGCTGATCTGGCACATTTGTTGGTGTGATGTTGAACTGCGCG 62
QY 573 CATAGTGAAGTGCACAAAGCAAGAGGAGGAGA 605

Db 61 CGTTCGGCGCGCGGAGGAGGAGGAGGGA 29

RESULT 13

US-10-259-165-41/c

Sequence 41, Application US/10259165

Publication No. US20030135888A1

GENERAL INFORMATION:

APPLICANT: Zhu, Tong

APPLICANT: Wang, Xun

APPLICANT: Chang, Hur-song

APPLICANT: Briggs, Steven P.

APPLICANT: Cooper, Bret

APPLICANT: Glazebrook, Jane

APPLICANT: Goff, Stephen A.

APPLICANT: Katagiri, Fumiaki

APPLICANT: Kreps, Joel

APPLICANT: Moughamer, Todd

APPLICANT: Provart, Nicholas

APPLICANT: Ricke, Darrell

TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

FILE REFERENCE: 70030-NP

CURRENT APPLICATION NUMBER: US/10/259,165

CURRENT FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/370,620

PRIOR FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/368,327

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 782

SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta

SEQ ID NO 41

LENGTH: 720

TYPE: DNA

ORGANISM: Oryza sativa

US-10-259-165-41

Query Match 8.6%; Score 137.4; DB 15; Length 720;

Best Local Similarity 56.9%; Pred. No. 2.4e-20;

Matches 292; Conservative 0; Mismatches 216; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTGTTGCTCTCCAAATGTTGTTACAGGATTGTTACATCTCCGGGTAC 157
DB 541 GGTGCAAGTACTGTTGCTCTCCAAATGTTGTTACAGGATTGTTACATCTCCGGGTAC 482
QY 158 TTTAAGTTGACACGGCAATCCACATTTATATTTGCTGCTGCAATGTAATTGTG----TGGC 213
DB 481 CCTCAGCTGCTCGGGCACTGCCCGGCACTGCTGCTGCTGCAACGGCGGCGCCCTTGGC 422
QY 214 ATTTCCCTCCACTTGGATTAGTCGGGGGAAAGTATCGGTATATTAATCCATCAACTA 273
DB 421 GCACCCGGCGCGTCCGGCGGGGAGGAAAGTCCATGGGCACGTTGAATCCGTCGATGA 362
QY 274 AAGAATGTCACCAATCTAAGTTGTTGAACTGCTCCAGGCGTACTCGGCTAGGGTGT 333
DB 361 GGGAGATGTCGAAGAAGTCGAGGTTGCTGAACTGTTTTCAGCGCAATCTCGCCAGCGTGT 302
QY 334 TTGTTGTTTTCGCCCAACCCCGTGCATCTGAGGACACCAACCAATCAACGATCATGACG 393
DB 301 TGGCGGCTGCCCGTACGCGCGCACCGCGCACCGCGCGCGTCTGCGCAC 242
QY 394 AACCTCTACAGCACCATCGAAGTTATCTCAGTACGACCCCATATACCTGCCATCGTAG 453
DB 241 GCCCGTTGCCCGTCCGCTGCAAGTGTGACGCGCGTCCGCGCCCAACGCGCGCCGCTCG 182
QY 454 TGCCCTTAGGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTCGGCACCGC-CATT 512
DB 181 TGCCCGCGGACGCTCGATCACCACCTGCTGCCCGGCTCCAGTCTGTCGCCCGCGCGG 122
QY 513 TCGGGTTCGATGCGGCCCAACAGATGATGACAGTGTTCGCGTACCTCGATAGTGGCAG 572
DB 121 ACGGCACGCGCTGCCCGCCACACGCGTGTCTGGCACTTGTGGTATGATGATGATGCGG 62

QY 573 CATRAGTGAAGTCAAAAAAGCAAGAGGGAGA 605
DB 61 CGTTCGGCGCGCGGAGGAGGAGGAGGGA 29

RESULT 14

US-10-437-963-86607/c

Sequence 86607, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 86607

LENGTH: 1006

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MBT4530_85631C.1

US-10-437-963-86607

Query Match 8.5%; Score 135.2; DB 17; Length 1006;

Best Local Similarity 56.6%; Pred. No. 9e-20;

Matches 290; Conservative 0; Mismatches 218; Indels 4; Gaps 2;

QY 98 GGTGCAACAATATTGTTGCTCTCCAAATGTTGTTACAGGATTGTTACATCTCCGGGTAC 157
DB 584 GGTGCAAGTACTGTTGCTCTCCAAATGTTGTTACAGGATTGTTACATCTCCGGGTAC 525
QY 158 TTTAAGTTGACACGGCAATCCACATTTATATTTGCTGCTGCAATGTAATTGTG---TGGCA 214
DB 524 CCTCAGCTGCTCGGGCACTGCCCGGCACTGCTGCTGCTGCAACGGCGGCGCCCTTGGC 465
QY 215 TTTCCCTCCACTTGGATTAGTCGGGGGAAAGTATCGGTATATTAATCCATCAACTAA 274
DB 464 GCACCCGGCGCGTCCGGCGGGGAGGAAAGTCCATGGGCACGTTGAATCCGTCGATGAG 405
QY 275 AAGAATGTCACCAATCTAAGTTGTTGAACTGGTCCAGGCGTACTCGGCTAGGGTGT 334
DB 404 GGAGATGTCGAAGAAGTCGAGGTTGCTGAACTGGTTTACGCGGCACTCCGCCAGCGTGT 345
QY 335 TGTGTTGTTTGGCCCAACCCCGTGCATCTGCAAGGACACCAACCAATCAACGTCATGCA 394
DB 344 GGGCGGCTGCCCGTACGCGCGCACCGGACGACGCGCGGCGGCGGCTGCGCACCG 285
QY 395 ACCTCTACAGCACCATCGAAGTTACATCCAGTACGAGCCCATATACCTGCCATCGTACT 454
DB 284 CCGTTTGGCGTCCGCTCGAAGTGTGAGCCCGTGGCGGCCACACGCGCCCGCCGCTGT 225
QY 455 GCCCTTAGGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTCGGCACCGC-CATT 513
DB 224 GCGGCGGCGACGTCGATCACCACCTGCTGCCCGGTTCCAGTCTGCGCGCGCGCGGA 165
QY 514 CGGGGTGATGCGGCCCAACGATGATGACAGTGTGCGTACCTCGATAGTGGCAGC 573
DB 164 CGGCACGCGTCCGCGCCACACGCGTGTCTGGCACTTGTGGTATGATGATGATGCGGCG 105
QY 574 ATAAGTGAAGTCAAAAAAGCAAGAGGGAGA 605
DB 104 GTTCGCGGCGCGGAGGAGGAGGAGGGA 73

Search completed: August 18, 2004, 16:52:35
Job time : 708.41 secs

RESULT 15
US-10-424-599-7736/C
; Sequence 7736, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7736
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ..(1173)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106998C.1
US-10-424-599-7736

Query Match 8.3%; Score 132; DB 13; Length 1173;
Best Local Similarity 57.0%; Pred. No. 5.1e-19;
Matches 311; Conservative 0; Mismatches 215; Indels 20; Gaps 3;

QY 49 ATCTTTGTTGAAATAATCGAAAGAACGTAGGACACACA-----TGGACCTTGGGTGC 102
Db 664 ACCTCTCTTTGAAGAACTTGGATAATCACTGGGACCGCAACCCGCGAGCCGGTGTCTAC 605

QY 103 AACAAATATCTGTCTCCCAATGTGGTACAGGATTTAGATCTCTCGGGTACTTTAA 162
Db 604 AACAGTACTGAGTCGTATTGAAACCGTGACGGGTGTGACGGCCGCGGAACCTGAA 545

QY 163 GTTGACCGAGGGCATTCACCATTTATATTTGCCGTGCATTGAATTTGGCGCATTTCCCTC 222
Db 544 GCTGAGTGGGACACTCTCCGATGATGTGGGCGCGCATTTACGGAGCTGCAGTTG---- 489

QY 223 CACTTGAATTAGTCGGGGCGAAAGTCATCGGTATATTAATTCATCAACTAAGAAATGT 282
Db 488 -----TAGGTGCGGGCTCACCTGCAAGGGAATGTTGAACCGTCCAGGGAGATGT 437

QY 283 CCCAGAAATCTAAGTTGTGAACTGGTCCAAAGCGTACTCGGTAGGGTGTGTTGGTGT 342
Db 436 CGTAGAGTCGAGGTTGTTGTACTGTTTCAACGGGAATTCACACAGTGTTCGGAGGTG 377

QY 343 TGCCTCCACCCGGTGCACGTGAGGACACCAACAATCACAGTCATGCAAGAACCTCTAC 402
Db 376 TACCTGTTTTTTGCACTCAAGAACACCCGTGCGAGTCGCGGTGAGGCACCTTCCCGCGTC 317

QY 403 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATCTGCCATCGTAGTCCCCCTAG 462
Db 316 CTGCGTTGTGCAAGGTGCGAGTTTGTTCGACCCCGAGATGCTCTCTCTGTCGTCGCTTGG 257

QY 463 GCGCATCAATGACCCACATTTGGCCCGCATTCGAAAGCTCGGACCCCGTTCGCGGTGGA 522
Db 256 TCACGCTGATGTTCCACGATTCGCCAGGTTAAGCCTTGAGCCGCGC--CGGGCACCGC 199

QY 523 TCGCCGCCAACGATGATGAGCAGTTGTTGGTACCTCGATAGTGGAGCATTAAGTGAA 582
Db 198 GCGGCCCAACACCGTGTAGTGCAATTTGTTGATGTTGAAGTTGCTGCTCGCTGAGCTAC 139

QY 583 AGTCAC 588
Db 138 GGCCAC 133

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 6041.75 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
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- 41: em.htgo.other.*

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and is derived by analysis of the total score distribution.

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2	1482.2	92.9	1598	6	AX665979	AX665979 Sequence
3	1362.4	85.4	1546	6	AX665980	AX665980 Sequence
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C 5	545	34.2	2638	8	SC13OLP	X72928 S.commerson
C 6	532	33.4	1304	8	AF093743	AF093743 Lycopersi
C 7	491	30.8	901	8	SC05MLP	X67121 S.commerson
C 8	480.2	30.1	2033	8	NTOSPR	X95308 N.tabacum o
C 9	479.2	30.0	1549	8	NTAP24G	X65701 N.tabacum a
C 10	479.2	30.0	3033	6	AR037158	AR037158 Sequence
C 11	479.2	30.0	3033	8	S40046	S40046 abscisic ac
C 12	463.6	29.1	818	8	AY007309	AY007309 Solanum d
C 13	463.4	29.1	729	8	AF473702	AF473702 Solanum n
C 14	463.2	29.0	917	8	AY093595	AY093595 Lycopersi
C 15	463	29.0	744	8	AF450276	AF450276 Solanum n
C 16	460.2	28.9	977	8	SCA81OLP	X72926 S.commerson
C 17	458.6	28.8	937	8	AF297646	AF297646 Capsicum
C 18	456.4	28.6	856	8	CAN297410	AJ297410 Capsicum
C 19	438.6	27.5	832	8	LETEMIM	X66416 L.esculentu
C 20	430.2	27.0	883	6	AL6780	AL6780 osmotin-lik
C 21	430.2	27.0	883	6	AR027097	AR027097 Sequence
C 22	430.2	27.0	883	6	AR103205	AR103205 Sequence
C 23	430.2	27.0	884	6	AL6782	AL6782 osmotin-lik
C 24	430.2	27.0	884	6	AR027098	AR027098 Sequence
C 25	430.2	27.0	884	6	AR103206	AR103206 Sequence
C 26	430.2	27.0	961	8	NTAP24	X65700 N.tabacum m
C 27	429.4	26.9	845	8	LEFRPA	X70787 L.esculentu
C 28	428.2	26.8	741	6	A83550	A83550 Sequence 1
C 29	428.2	26.8	741	6	BD082734	BD082734 Antifunga
C 30	424.4	26.6	928	8	S44889	S44889 osmotin=pat
C 31	421.4	26.4	917	8	TOMNP24	M21346 Tomato NP24
C 32	409.2	25.7	971	8	AF376058	AF376058 Petunia x
C 33	404.2	25.3	738	8	NTOSMOTIN	X61679 N.tabacum m
C 34	399	25.0	541	8	AY256440	AY256440 Solanum t
C 35	398.8	25.0	542	8	AY256441	AY256441 Solanum t
C 36	398.6	25.0	526	8	AY256436	AY256436 Solanum t
C 37	398.2	25.0	593	8	AY256429	AY256429 Solanum t
C 38	397.8	24.9	567	8	AY256439	AY256439 Solanum t
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C 41	394	24.7	510	8	AY256425	AY256425 Solanum t
C 42	392.4	24.6	539	8	AY256430	AY256430 Solanum t
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C 44	385.8	24.2	3127	8	TOBNP50	D76437 Nicotiana s
C 45	384.6	24.1	541	8	AY256428	AY256428 Solanum t

ALIGNMENTS

RESULT 1
AX665978
LOCUS AX665978 1595 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1 from Patent WO02059333.
ACCESSION AX665978
VERSION AX665978.1 GI:29290847
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
TITLE Gene promoters isolated from potato and use thereof

Pred. No. is the number of results predicted by chance to have a


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Query Match      92.9%; Score 1482.2; DB 6; Length 1598;
Best Local Similarity 96.7%; Pred. No. 1.8e-285;
Matches 1546; Conservative 0; Mismatches 48; Indels 5; Gaps 3;

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DB 121 CAATTTGTTGCAAGGATTTTACATCTCCGGTACTTTAAGTTGACCGGCAATTCAC 180
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QY 839 ATATAGCCTATAGTTACAAAGTTAACTTTATTTGTTGATGAATTTGACATATAACTCTGT 898
DB 841 ATATAGCCTATAGTTACAAAGTTAACTTTATTTGTTGATGAATTTGACATATAACTCTGT 900
QY 899 AACGTGACGGAATTTTCTTAAACTAAATATTAAGAGCGCTATTTTCAGATTTTCG 958
DB 901 AACGTGACGGAATTTTCTTAAACTAAATATTAAGAGCGCTATTTTTCAGATTTTCG 960
QY 959 TGGCCAAAGTTTCTTGCACTATCTATGATGCCATTTTATCTTTTATGCTTACGCTTC 1018
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QY 1139 TTTAAAAATCACAAACCATCTTCC--AAGGGGAAGTCTATGTGATCCGTGACAAGTGGTTT 1196
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DB 1200 GAATTTCTTAGTCTAGATTTGAGTACAACTTTTAGTGCATAATCTATTAAGAAGAAC 1259
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DB 1260 CTTATTGATGCAATATCTATTAAGAAAGACCCCTATTCATGCTTTATTTTATTTTACGAT 1319
QY 1317 CGAGCATGGAATATATTTACTAATTAATAAATAAATTTGGAAGGAATTTGATCGACAAGTCACT 1376
DB 1320 CGAGCATGGAATATATTTACTAATTAATAAATAAATTTGGAAGGAATTTGATCGACAAGTCACT 1379
QY 1377 AAGCTTATCGTCGATCCCACTTAATAACGTTAGTATGGCTGCTTTTAGAGAAACAAGT 1436
DB 1380 AAGCTTATCGTCGATCCCACTTAATAACGTTAGTATGGCTGCTTTTAGAGAAACAAGT 1439
QY 1437 GGATCATGTATTAATTTAGTTTAAATATCTCTATAAATATCTATATATATACCTCTAA 1496
DB 1440 GGATCATGTATTAATTTAGTTTAAATATCTCTATAAATATCTCTATATCTCTTAA 1499
QY 1497 CTAAATGCACTTAACACCAATATTAACCTTAGATCTTTTAAAGAAATTTGAGAAATTA 1556
DB 1500 CCAAAATACATCTAAACACCAATATTAACCTTAGATCTTTTAAAGAAATTTGAGAAATTA 1559
QY 1557 ATGGAGGCAAAATAAGTCTATGTTGAAAGTTGTTGCTTTC 1595
DB 1560 ATGGAGGCAAAATAAGTCTATGTTGAAAGTTGTTGCTTTC 1598

RESULT 3
LOCUS      AX665980      1546 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02059333.
ACCESSION  AX665980
VERSION     AX665980.1  GI:29290849
KEYWORDS
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE   1
AUTHORS     Dai, Z., Shi, L. and Hooker, B.S.
TITLE       Gene promoters isolated from potato and use thereof
JOURNAL     Patent: WO 02059333-A 3 01-AUG-2002;
            Dai, Ziyu (US) ; Shi, Lifang (US) ; Hooker, Brian, S. (US)
FEATURES
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            1..1546
            /organism="Solanum tuberosum"
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Query Match      85.4%; Score 1362.4; DB 6; Length 1546;
Best Local Similarity 94.1%; Pred. No. 1.4e-261;
Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

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DB 1 ATCTTTGTTGAAAAAATTTGAAAAAGACCTAGGACCAATGACCTTGGGTGCAACAT 60
QY 109 ATTGTTGTCCTCCAAATGTTGTTACAGGATTTGTTACATCCTCGGGTACTTTAAGTTGAC 168
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ORIGIN

Query Match	45.1%;	Score 718.6;	DB 8;	Length 2659;
Best Local Similarity	74.3%;	Pred. No. 3.6e-133;		
Matches 1166;	Conservative 0;	Mismatches 189;	Indels 214;	Gaps 12;
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DB	1675	GGCATCTTTTCTTGAAAAATTTGGACAACCTCTGTAGGACACCATGGACCTTGGTGCAC	1616	
QY	106	AATATTGTTGTCCTCCAAATGTGGTGAACAAGATTGTTACATCTCTCCGGGTACCTTTAAGTT	165	
DB	1615	AATATTGTTGTCCTCCAAACGTGGTGAACAAGATTGTTACATCTCTCCAGGTACCTTAAGG	1556	
QY	166	GACCAGGGCATTCACCATTTTATATTTCGGGTGCATGAATTGTGTGCATTTCCCTCCAC	225	
DB	1555	CGCAGGACATTCACCATTTTATATTGCGCGTGCATGAATTGTGTGCATTTCCAGCAC	1496	
QY	226	TTTGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCTC	285	
DB	1495	TAGGTTTGGTCGGGGCAAAAGTCATTGGAATATTGAATCCGTCACTAAAGAAATATCCC	1436	
QY	286	AGAAATCTAAGTTGTTGAACTGTGTCGAAGGGTACTCGGCTAGGGTGTTTGGTGTGCTGC	345	
DB	1435	AGAAATCTAGGTGCTCTAACTGATCCTCAAGGCATATTCCAGCCAAGGTGTTTGGGGGCTTAC	1376	
QY	346	CCCACCCGGTGCACCTGCAGGACACCAACAATCACCAGTCATGCACGAACCTCTACCGAG	405	
DB	1375	CCCACCCGGTACACTGCAGACTCCACCAATCACCAGTCTGACAGAACCCCTTCTCTG	1316	
QY	406	CAACATCGAAGTTACATCCAGTACGACCCCAATATACCTGCGCATCGTATAGTCGCCCTAGCG	465	
DB	1315	CAGCATTTGAAGTTACAAACCACTAGTACGACCCCATATACGTGCGCATCTTAGTTCCCTCTGGAG	1256	
QY	466	CATCAATGACCCCATTTGCGCCCGATCGAAACGTGCG - GCACCGCTTTCGGGGTCCGATG	524	
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QY	525	CCGCCCAAAACGATGATGGACAGTTGTGCGTACTCTCGATAGTGGCAGCATAAGTGAAG	584	
DB	1195	CTGCCACACGGTGTATGGACAGTTGTGGTACCTCGATAGTCGACAGCATAGTGTGAAG	1136	
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DB	1135	TCACAAAGACNAGAGGAGGAGAAATAAAGAGATCTCAAGTAGCCCATGTTAATGTGTT	1076	
QY	641	GAATTTATATGTGGACAAATTAATTTTGGTACTTTATATATAGGATATGGCGGCTTTT	700	
DB	1075	GAATTTATATGAGGACAAATTAATTTTGGTACTTT - TATATAGGGGTATGGCGGCTTTT	1017	
QY	701	GGCACTACGGATATTAAT - CGTATTATATAGCAATATACATCTTTGACTAATATATAA	757	
DB	1016	GGCACTATGGATTTTATTAATCATATATAACACAGTATCATACTTTGATTAATATAA	957	
QY	758	CGAATATATTACAAATATGATTTTGGTAAAAGTTTCAGGTGGGAAAATCTATAAGACCGCC	817	
DB	956	CGAAAAATATTAAATATATGCGTTGGTAAAGGTTTGAAG - TAAAGACCGCC	909	
QY	818	TAATAATTAATTAATTTTATGAATATAGCCTATAGTTTAACTTTATTTTGGTGATA	877	
DB	908	TAATAATTAATTAATTTTATG - TAAAGACCGCC	889	
QY	878	ACTTTGACATATAAAGTCTGTGAAGTGAAGGAAATTTTCTTAAACATAATATTT -	931	
DB	888	-----AACTCTGTGAAGTGAAGGAAATTTTCTTAAACATAATATTTTCTTTA	842	
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QY	1108	GATCAATCTGAAATATACAAACCAATCTGATTTTAAATAACACACCAATCTCTGCCAAGGG	1167
DB	670	GATTAAACATGAAATATACAAATCAACACGATTTTGTATGTAACAGATCATTTG-----	619
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DB	618	-----TTGGACCACCAACT	606
QY	1228	TTTGTAGTGCRAATATCTATTAAAAAGAACCCCTATTGTATGCAAAATATCTATTAAAAAGAAC	1287
DB	605	TTTAAATCCAGTAGTATCTATTAAAAAGAACCCCTATTGTATGCAAAATCAAT-----	556
QY	1288	CCTATTCAATGCTTTATTATTTTACGATCGGACCATGGATATATTACTTAATTAATAATA	1347
DB	555	-----AAATA	555
QY	1348	AATTGGAGGAATATGATCGCAAGTCATCAAGCTTATCGTCGATCCACATTAATAATAACG	1407
DB	550	AATTGGGAGGATGATGACAAAGTCATCAAACTTATCGTCGATCCACATTAATAATAATG	491
QY	1408	TTAGTATGGCTGCTTTTAGAGAAAACAAGATGGATCATGTAATTAATTTAGTT-TTAAAAATATC	1466
DB	490	TTAGTATGGCTGCTTTTAGAGTAAACAAGATGGATCATGCTACAAATTTAGTTAAAAAAATATC	431
QY	1467	TCCTATAAATATCTATATATATACCTCTAAACCTAAATGATCATCTAACACACAAAAATATAAC	1596
DB	430	TCCTATAAATATATATCTATACCTCTAAACCTAAATGATCATCTAACACACAAAAATATAAC	371
QY	1527	TTAGATCTTTTAAAGAAATTGACAGATTAATAATGAGGCAATAAGTCTATGGTGAAGTTG	1586
DB	370	TTAGATCTTTTAAAGAAATTGACAGATTAATAATGAGGCAATAAGTCTATGGTGAAGTTG	311
QY	1587	GTTCGTTTC	1595
DB	310	GTTCGTTTC	302
RESULT 5			
LOCUS	SC130LP/c		
DEFINITION	S commersonii (pOSML13) gene for osmotin-like protein.	DNA linear	PLN 27-OCT-1999
ACCESSION	X72928		
VERSION	X72928.1	GI:296771	
KEYWORDS	osmotin-like protein.		
SOURCE	Solanum commersonii (Commerson's wild potato)		
ORGANISM	Solanum commersonii		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	Zhu, B., Chen, T.H. and Li, P.H.		
TITLE	Activation of two osmotin-like protein genes by abiotic stimuli and fungal pathogen in transgenic potato plants		
JOURNAL	Plant Physiol. 108 (3), 929-937 (1995)		
MEDLINE	95357444		
PUBMED	7630973		
REFERENCE	2 (bases 1 to 2638)		
AUTHORS	Zhu, B.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA		
COMMENT	Related sequences: M29279 & M21346.		
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Qy      585  TCACAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTGAA 643
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RESULT 8
NTOSPR/c
LOCUS   NTOSPR N.tabacum osmotin gene. 2033 bp DNA linear PLN 01-FEB-1996
DEFINITION
ACCESSION X95308
VERSION X95308.1 GI:1167853
KEYWORDS osmotin; PR protein.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1
REFERENCE
AUTHORS Barnard, W.M. and Neale, A.D.
TITLE Comparison of the 5 regulatory regions of homeologous osmotin genes
from Nicotiana tabacum
JOURNAL Unpublished
AUTHORS Neale, A.D.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1996) A.D. Neale, Monash University, Genetics and
Developmental Biology, Wellington Rd, Clayton, Victoria, 3168,
Australia

FEATURES
source Location/Qualifiers
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Db      1325  CATTGATCACCCAAAGTTTGGCTCGATCGAGGCGTCGGCCACCGCCTATGGGGTCGACG 1266

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DEFINITION
ACCESSION X65701
VERSION X65701.1 GI:19782
KEYWORDS osmotin.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
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REFERENCE
AUTHORS Melchers, L.S., Sela-Buurlage, M.B., Vloemans, S.A., Woloshuk, C.P.,
Van Roekel, J.S., Pen, J., van den Elzen, P.J. and Cornelissen, B.J.
TITLE Extracellular targeting of the vacuolar tobacco proteins AP24,
chitinase and beta-1,3-glucanase in transgenic plants
JOURNAL Plant Mol. Biol. 21 (4), 583-593 (1993)
MEDLINE 93192519
PUBMED 8448358
REFERENCE
AUTHORS Melchers, L.S.
TITLE Direct Submission

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JOURNAL Submitted (24-APR-1992) L.S. Melchers, Mogen International NV,
Einsteinweg 97, 2333 CB Leiden, THE NETHERLANDS

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Best Local Similarity 76.9%; Pred. No. 2e-85;
Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;

Qy 46 GGTATCTTTGTTGAAAAAATTTGAAAAAGAACGTAGGACCAACATGGACCTTGGGTGCAAC 105
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LOCUS AR037158 3033 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5801028.
ACCESSION AR037158
VERSION AR037158.1 GI:5955014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3033)
AUTHORS Bressan,R. and Hasegawa,P.M.
TITLE Osmotin gene promoter and use thereof
JOURNAL Patent: US 5801028-A 1 01-SEP-1999;
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Query Match 30.0%; Score 479.2; DB 6; Length 3033;
Best Local Similarity 76.9%; Pred. No. 2e-85;
Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;

Qy 46 GGTATCTTTGTTGAAAAAATTTGAAAAAATGTAGGACCAACATGGACCTTGGGTGCAAC 105
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Qy 106 AATATTGTTGTCCTCCAAATGTGTACAGGATTTGTACATCTCCCGGTACTTTAAGTT 165
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LOCUS Solanum dulcamara cryoprotective osmotin-like protein mRNA,
DEFINITION complete cds.
ACCESSION AY007309
VERSION AY007309.1 GI:10445202
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 818)
AUTHORS Newton,S.S. and Duman,J.G.
TITLE An osmotin-like cryoprotective protein from the bittersweet
nightshade Solanum dulcamara
JOURNAL Plant Mol. Biol. 44 (5), 581-589 (2000)
MEDLINE 21039368
PUBMED 11198420
REFERENCE 2 (bases 1 to 818)
AUTHORS Newton,S.S. and Duman,J.G.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Biological Sciences, University of Notre
Dame, Galvin Life Sciences Bldg., Notre Dame, IN 46556, USA
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RESULT 13
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DEFINITION AF473702
ACCESSION AF473702.1 GI:18874518
VERSION
KEYWORDS
SOURCE
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Solanum nigrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 729)
AUTHORS Jami,S.K. and Kirti,P.B.
TITLE PCR-based cloning of an osmotin-like protein gene from Solanum
nigrum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 729)
AUTHORS Jami,S.K. and Kirti,P.B.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2002) Department of Plant Sciences, University of
Hyderabad, Gachibowli, Hyderabad, A.P 500046, India
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ACCESSION AF450276
VERSION AF450276.1 GI:19401630
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 744)
AUTHORS Campos,M.A., Ribeiro,S.G., Rigden,D.J., Monte,D.C. and Grossi de Sa,M.F.
TITLE Pathogenesis related-like genes of Solanum nigrum: cloning and characterization of genes coding for neutral and basic PR5-like proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 744)
AUTHORS Campos,M.A., Ribeiro,S.G., Monte,D.C. and Grossi de Sa,M.F.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2001) PBI, Embrapa Genetic Resources and Biotechnology, P.O. Box 02372, Brasilia, DF 70770-900, Brazil
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	362.2	22.7	1004	2	Aaq21414 Encodes o
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13	195.6	12.3	735	7	Abz42096 Arabidops
14	195.6	12.3	735	7	Ada68525 Arabidops
15	195.6	12.3	950	6	Abn98566 Arabidops
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17	166.8	10.5	771	3	Aaz23511 Asparagus
18	155.2	9.7	900	1	Aan90842 Fragment
19	155.2	9.7	900	2	Aav62808 Tobacco P
20	155.2	9.7	900	2	Aav72992 PR-R major
21	149	9.3	910	4	Aad04241 Sunflower
22	146.8	9.2	549	3	Aac55150 Arabidops
23	128.6	8.1	500	3	Aaa40422 Potato in

ALIGNMENTS

RESULT 1
ABK90560

ID ABK90560 standard; DNA; 1595 BP.

XX XX

AC ABK90560;

XX XX

DT 15-NOV-2002 (first entry)

XX XX

DE DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform 1.

XX XX

KW KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;

KW KW Controlled Environmental Agriculture; crop cultivation.

XX XX

OS Solanum tuberosum.

XX XX

PN WO200259333-A2.

XX XX

PD 01-AUG-2002.

XX XX

PF 18-JAN-2002; 2002WO-US001287.

XX XX

PR 23-JAN-2001; 2001US-0263224P.

XX XX

PA (DAIZ/) DAI Z.

PA (SHIL/) SHI L.

PA (HOOK/) HOOKER B S.

XX XX

PI Dai Z, Shi L, Hooker BS;

XX XX

DR WPI; 2002-608457/65.

XX XX

PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes and in Controlled Environmental Agriculture for heterologous protein production.

PT PT

PS Claim 2; Fig 1; 43pp; English.

XX XX

CC The invention relates to polynucleotides having proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1 (pin1) or aminotransferase (amt) gene promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in Controlled Environmental Agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms

CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform
 XX
 SQ Sequence 1595 BP; 510 A; 291 C; 297 G; 497 T; 0 U; 0 Other;

Query Match	99.9%;	Score 1593.4;	DB 6;	Length 1595;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1594;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	GTAATACGACTCACTATAGGACGCGTGTGTCAGCGCCCTGGCTGCTGTTGTTTGA	60	
DB	1	GTAATACGACTCACTATAGGACGCGTGTGTCAGCGCCCTGGCTGCTGTTGTTTGA	60	
QY	61	AAAAATGGAAAGAAAGTGGAGACCAATGAGACCTTTGGGTGCAACAATATTTGTGCTTC	120	
DB	61	AAAAATGGAAAGAAAGTGGAGACCAATGAGACCTTTGGGTGCAACAATATTTGTGCTTC	120	
QY	121	CAATGTGTGACAGGATTGTTACATCTCCGGGTACTTTTAACTTACACGAGGCAATTCAC	180	
DB	121	CAATGTGTGACAGGATTGTTACATCTCCGGGTACTTTTAACTTACACGAGGCAATTCAC	180	
QY	181	CAATTTATATTTGGCGTGCATTTGTTGGCAATTTCCCTCCACTTGGATTAGTCGGGG	240	
DB	181	CAATTTATATTTGGCGTGCATTTGTTGGCAATTTCCCTCCACTTGGATTAGTCGGGG	240	
QY	241	CGAAGTCATCGGTATATTAATCCATCACTAAAGAAATGTCACAGAAATCTAAGTTGT	300	
DB	241	CGAAGTCATCGGTATATTAATCCATCACTAAAGAAATGTCACAGAAATCTAAGTTGT	300	
QY	301	TGAACCTGTCACAGGCGTACTCGGCTAGGCGTGTGTTGGTGGTTTCCGCCACCGGTCAC	360	
DB	301	TGAACCTGTCACAGGCGTACTCGGCTAGGCGTGTGTTGGTGGTTTCCGCCACCGGTCAC	360	
QY	361	GCAGGACACCAACCAATACCAAGTCATGCAAGAACTCTTACAGCAACCATCGAAGTTAC	420	
DB	361	GCAGGACACCAACCAATACCAAGTCATGCAAGAACTCTTACAGCAACCATCGAAGTTAC	420	
QY	421	ATCCAGTACGACCCCATATACCTGCTGCTAGTGGCCCTAGGCGCATCAATGACCCACA	480	
DB	421	ATCCAGTACGACCCCATATACCTGCTGCTAGTGGCCCTAGGCGCATCAATGACCCACA	480	
QY	481	TTTGGCCCGCATCGAAGCTCGGACCCGCTTTTGGGGTGTGATGCGCCGCAACGATGTA	540	
DB	481	TTTGGCCCGCATCGAAGCTCGGACCCGCTTTTGGGGTGTGATGCGCCGCAACGATGTA	540	
QY	541	TGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCACAAAGCAAGAAG	600	
DB	541	TGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCACAAAGCAAGAAG	600	
QY	601	GGAGAAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTCGACAAA	660	
DB	601	GGAGAAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTCGACAAA	660	
QY	661	TTATTTTGGTACTTTATATATAGGATATGGCGCTTTGGCCTACGCGATTAATCG	720	
DB	661	TTATTTTGGTACTTTATATATAGGATATGGCGCTTTGGCCTACGCGATTAATCG	720	
QY	721	TATTTATAGCAATATCATATCTTTGACTAATTAACGAAATATATTAATATGATGTTT	780	
DB	721	TATTTATAGCAATATCATATCTTTGACTAATTAACGAAATATATTAATATGATGTTT	780	
QY	781	GGTAACCGTTGAGGTGGAATAATGTTAAGAGCCGCTAATAATTAATTAATTAATGAT	840	
DB	781	GGTAACCGTTGAGGTGGAATAATGTTAAGAGCCGCTAATAATTAATTAATTAATGAT	840	
QY	841	ATAGCCTATAGTTACAGTTAACTTTATTTTGGTGATACTTTTGACATATAAATCTCGTAA	900	
DB	841	ATAGCCTATAGTTACAGTTAACTTTATTTTGGTGATACTTTTGACATATAAATCTCGTAA	900	
QY	901	CGTGACGGAATTTTTCTTAAACCTAAATATTAATAAGACGAGCTATTTTCAGATTTTCGTG	960	
DB	901	CGTGACGGAATTTTTCTTAAACCTAAATATTAATAAGACGAGCTATTTTCAGATTTTCGTG	960	

RESULT 2

ABK90561
 ID ABK90561 standard; DNA; 1598 BP.

XX AC ABK90561;
 XX DT 15-NOV-2002 (first entry)
 XX DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform II.
 XX KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
 KW Controlled Environmental Agriculture; crop cultivation.
 XX OS Solanum tuberosum.
 XX PN WO200259333-A2.
 XX PD 01-AUG-2002.
 XX PF 18-JAN-2002; 2002WO-US001287.
 XX PR 23-JAN-2001; 2001US-0263224P.
 XX PA (DAIZ/) DAI Z.
 XX PA (SHIL/) SHI L.
 XX XX (HOOK/) HOOKER B S.

PI Dai 2, Shi L, Hooker BS;
 XX WPI; 2002-608457/65.
 XX
 PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
 PT isoforms derived from potato, useful in manipulating expression of genes
 PT and in Controlled Environmental Agriculture for heterologous protein
 PT production.
 XX
 PS Claim 2; Fig 2; 43pp; English.
 CC
 CC The invention relates to polynucleotides having proteinase inhibitor 1
 CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
 CC and amt gene promoters are useful in manipulating expression of genes
 CC particularly in transformed plant cells. The gene promoters are useful in
 CC constructing gene expression vectors and in Controlled Environmental
 CC Agriculture for heterologous protein production. The vectors are useful
 CC in facilitating the expression and/or secretion of heterologous proteins
 CC in cell culture or by crop cultivation. The new gene promoter isoforms
 CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform
 XX
 SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;
 Query Match 93.0%; Score 1483.8; DB 6; Length 1598;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 1547; Conservative 0; Mismatches 47; Indels 5; Gaps 3;
 1 GTAATAGACTCACTATAGGCGACGGTGGTTCGACGGCCCTGCTGGTATCTTTGTTGA 60
 1 GTAATAGACTCACTATAGGCGACGGTGGTTCGACGGCCCGGGCTGGTATCTTTGTTGA 60
 61 AAAAAATGGAAAGAACTAGGACCAATGACCTTGGGTGGCAACATATTTGTTCCCTC 120
 61 AAAAAATGGAAAGAACTAGGACCAATGACCTTGGGTGGCAACATATTTGTTCCCTC 120
 121 CAAATGGTACAAAGGATTTGTATCATCTCGGGTACTTTAAGTTGACCAAGGCAATTCAC 180
 121 CAAATGGTACAAAGGATTTGTATCATCTCGGGTACTTTAAGCTGACTAGGACATTCAC 180
 181 CATTATATTTGCGTGCATTAATGTTGGGCAATTTCCCTCCATTTGGATTAGTCGGGG 240
 181 CATTATATTTGCGTGCATTAATGTTGGGCAATTTCCCTCCATTTGGATTAGTCGGGG 240
 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCCTCAGAAATCTAAGTTGT 300
 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCCTCAGAAATCTAAGTTGT 300
 301 TGAATCGTCCAAAGCGTACTCGGCTAGGGTGTGTTGGTGGTTTCCGCCACCCGGTGCAC 360
 301 TGAATCGTCCAAAGCGTACTCGGCTAGGGTGTGTTGGTGGTTTCCGCCACCCGGTGCAC 360
 361 GCAGGACACCAACCAATCAGTGCATGACGAACTCTACAGCAACCTACAGCAACCTACG 420
 361 GCAGGACACCAACCAATCAGTGCATGACGAACTCTACAGCAACCTACAGCAACCTACG 420
 421 ATCCAGTACGACCCCATATATGTCGATGTCGAGCACTCTACAGCAACCTACAGCAAC 480
 421 ATCCAGTACGACCCCATATATGTCGATGTCGAGCACTCTACAGCAACCTACAGCAAC 480
 481 TTTGGCCCGGATCGAAACGTCGACCGCCGCTTTCGGGGTTCGATCGCGCCCAACGATGTA 540
 481 TTTGGCCCGGATCGAAACGTCGACCGCCGCTTTCGGGGTTCGATCGCGCCCAACGATGTA 540
 541 TGGCAGTTGTTG - CGTACCTCGATGTCGACGATGAAAGTCAAAAAAGCAAGA 598
 541 TGGCAGTTGTTGCGGGTACCTTCGATGTCGACGATGAAAGTCAAAAAAGCAAGA 600
 599 AGGGAGAAAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTGACA 658
 601 AGGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTGACA 660

QY 659 AATTATTTTGGTACTTTTATATAGGATATAGGCGCTTTTGGCACTACGATATTAAT 718
 DB 661 AATTATTTTGGTACTTTTATATAGGATATAGGCGCTTTTGGCACTACGATATTAAT 720
 QY 719 CGTATTATATAGCAATATCATATTTGACTTAATTAATAAGCAATATATTAATATATGAT 778
 DB 721 CGTATTATATACCAATATCATATTTGACTTAATTAATAAGCAATATATTAATATATGAT 780
 QY 779 TTGGTAAAGCTTGAAGTGGAAAAATGATATAGAGCCGCTAATAATTAATTAATTTATGA 838
 DB 781 TTGGTAAAGCTTGAAGTGGAAAAATGATATAGAGCCGCTAATAATTAATTTATGA 840
 QY 839 ATATAGCCTATATAGTTTACAAATTAATTTTATTTGGTGAATACTTTGACATATAAATCTGT 898
 DB 841 ATATAGCCTATATAGTTTACAAATTAATTTTATTTGGTGAATACTTTGACATATAAATCTGT 900
 QY 899 AACGTGACGGAATTTTCTTAAACTAAATTAATAAGCAAGCTATTTTTCAGATTTTCG 958
 DB 901 AACGTGACGGAATTTTCTTAAACTAAATTAATAAGCAAGCTATTTTTCAGATTTTCG 960
 QY 959 TGGCCAAAGTTTCTTGGCATACTTATCTATGCCCCATTTTACTTTTATCGTTCTAGCCCTC 1018
 DB 961 TGGCCAAAGTTTCTTGGCATACTTATCTATGCCCCATTTTACTTTTATCGTTCTAGCCCTC 1020
 QY 1019 TAGGTACAGCTTGAACATATAAATAATCATATAAATTAATAAGTAAATAATTTTATTTT 1078
 DB 1021 TAGGTACAGCTTGAACATATAAATAATCATATAAATTAATAAGTAAATAATTTTATTTT 1080
 QY 1079 TTCAATTTACTCGTAGGATCAATTTTGTAGTCAATCTGAATATACAAACCATTTCTGAT 1138
 DB 1081 TTCAATTTACTCGTAGGATCAATTTTGTAGTCAATCTGAATATACAAACCATTTCTGAT 1140
 QY 1139 TTTAAATACCAACCATTTCTGCC--AAGGGGAAGCTATGTGATCCGTGACAAGTGGTTT 1196
 DB 1141 TTTAAATACCAACCATTTCTGCCAATGCGGAAGCTATGTGATCCGTGGAAGT-GTTT 1199
 QY 1197 GATTATTTCTAGTCTAGATTTGGAGTCAACATTTTGTAGTCAATCTTAATAAGAAACC 1256
 DB 1200 GATTATTTCTAGTCTAGATTTGGAGTCAACATTTTGTAGTCAATCTTAATAAGAAACC 1259
 QY 1257 CTTATTTGATGCAATATCTTATTAAGAAACCCCTATTTCTATTTTATTTTATTTTACGAT 1316
 DB 1260 CTTATTTGATGCAATATCTTATTAAGAAACCCCTATTTCTATTTTATTTTACGAT 1319
 QY 1317 CGGAGCATGGATATATTTACTAATTAATAAATTTGGAAGGAATTTGATCGACAAGTCATC 1376
 DB 1320 CGGAGCATGGATATATTTACTAATTAATAAATTTGGAAGGAATTTGATCGACAAGTCATC 1379
 QY 1377 AAGCTTATCGTGCATCCACATTAATAAATACGTTAGTATGCGCTTTTATAGAAACCAAGT 1436
 DB 1380 AAGCTTATCGTGCATCCACATTAATAAATACGTTAGTATGCGCTTTTATAGAAACCAAGT 1439
 QY 1437 GGATCATGTATATTTAGTTTAAATATCTCTATAAATATCTCTATAAATACCTGTCTATCCCTTAA 1496
 DB 1440 GGATCATGTATATTTAGTTTAAATATCTCTATAAATATCTCTATAAATACCTGTCTATCCCTTAA 1499
 QY 1497 CTTAAATGCACTACAAACCAATATAAATCTTAGATTTCTTTAAAGAAATTTGCAAGTAA 1556
 DB 1500 CCAATATACATCTAACACAAATATAAATCTTAGATTTCTTTAAAGAAATTTGCAAGTAA 1559
 QY 1557 ATGGAGGCAAAATAGTCTATGTTGGAAGTTGGTTGCTTTC 1595
 DB 1560 ATGGAGGCAAAATAGTCTATGTTGGAAGTTGGTTGCTTTC 1598

RESULT 3
 ID ABK90562
 XX ABK90562 standard; DNA; 1546 BP.
 AC ABK90562;
 XX
 XX
 DT 15-NOV-2002 (first entry)
 XX

DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform III.

KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
Controlled Environmental Agriculture; crop cultivation.

XX Solanum tuberosum.

XX WO200259333-A2.

PN 01-AUG-2002.

PD 18-JAN-2002; 2002WO-US001287.

XX 23-JAN-2001; 2001US-0263224P.

PR (DAIZ/) DAI Z.

PA (SHIL/) SHI L.

XX (HOOK/) HOOKER B S.

PI Dai Z, Shi L, Hooker BS;

XX WPI; 2002-608457/65.

XX New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter

PT isoforms derived from potato, useful in manipulating expression of genes

PT and in Controlled Environmental Agriculture for heterologous protein

PT production.

XX Claim 2; Fig 3; 43pp; English.

XX The invention relates to polynucleotides having proteinase inhibitor 1
CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
CC and amt gene promoters are useful in manipulating expression of genes,
CC particularly in transformed plant cells. The gene promoters are useful in
CC constructing gene expression vectors and in Controlled Environmental
CC Agriculture for heterologous protein production. The vectors are useful
CC in facilitating the expression and/or secretion of heterologous proteins
CC in cell culture or by crop cultivation. The new gene promoter isoforms
CC provide high level, stable and controllable expression that is
CC temporally, environmentally, or developmentally regulatable. This
CC sequence represents a potato pin1 gene promoter isoform

XX SQ Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match 86.2%; Score 1375.2; DB 6; Length 1546;

Best Local Similarity 94.8%; Pred. No. 7.6e-293;

Matches 1469; Conservative 0; Mismatches 74; Indels 9; Gaps 4;

QY 49 ATCTTTGTTTGAATAAATTGGAAAGAAAGCTAGGACCATGACCTTGGGTGCAACAAT 108

DB 1 ATCTTTGTTTGAATAAATTGGAAAGAAAGCTAGGACCATGACCTTGGGTGCAACAAT 60

QY 109 ATGTTGTCCTCAATGTTGTTACAGGATGTTATCATCTCCGGGTACTTTAAGTGCAC 168

DB 61 ATGTTGTCCTCAATGTTGTTACAGGATGTTATCATCTCCGGGTACTTTAAGTGCAC 120

QY 169 CAGGGCATTCACCATTTATTTGCGTGCATTGAATTTGTTGGCATTTCCCTCCACCTG 228

DB 121 TAGGACATTCACCATTTATTTGCGTGCATTGAATTTGTTGGCATTTCCCTCCACCTG 180

QY 229 GATTAGTCGGGGGGAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGA 288

DB 181 GATTAGTCGGGGGGAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGA 240

QY 289 AATCTAAGTTGTTGAATCTGCTCAAGGCGTACTCGCTAGGCGTGTTCGTGGTTGCCCC 348

DB 241 AATCTAAGTTGTTGAATCTGCTCAAGGCGTACTCGCTAGGCGTGTTCGTGGTTGCCCC 300

QY 349 ACCGGTGCACCTGCAGGACACCAACAATCAACAGTCATGACGAACTCTACAGCAC 408

DB 301 ACCGGTGCACCTGCAGGACACCAACAATCAACAGTCATGACGAACTCTACAGCAC 360

QY 409 CATCGAAGTTACATCCAGTACGACCCCATATACCTGTCATCGTAGTCCCTTAGGGCAT 468

DB 361 CATCGAAGTTACATCGAATGACCCCATATACGTGCCATCGTAGTCCCTTAGGGCAT 420

QY 469 CAATGACCCACATTTGGCCCCGATCGAAACGTCGG-CAACCCGCTTTCCGGGTGCGATGCCG 527

DB 421 CAATGACCCACGTTTGGCCTCGATCGAGACGTCGGCCACCGCTATCGGGTGCATGCTG 480

QY 528 CCCAAGCATGTATGACAGTTGTTGCGTACTCTGATAGTGGCAGCATAAAGTGAATCA 587

DB 481 CCCAGACGCTGATGGAAGTTGTTGCGTACTCTGATAGTGGCAGCATAAAGTGAATCA 540

QY 588 CAAAAGCAAGAGGAGGAGAAACAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT 647

DB 541 CAAAAGCAAGAGGAGGAGAAACAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT 600

QY 648 ATATGTGACAAATTTATTTTGGTACTTTATATATAGGGATATGGCGCTTTTGGCACTA 707

DB 601 ATATGTGACAAATTTATTTTGGTACTTTATATATAGGGATATGGCGCTTTTGGCACTA 660

QY 708 CGGATATTAATCGTATTATATAGCAATATCATCTTTGACTTAATTAAGCAATATAT 767

DB 661 TGGATATTAATCGTATTATATACAAATATCATCTTTGACTTAATTAAGCAATATAT 720

QY 768 TACAATATGATTTGGTAAACGTTGAGGTGGAAATCTATAAGAGCCGCTTAATAATTA 827

DB 721 TACAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCCGCTTAATAATTA 780

QY 828 TTATTTATGAATATAGCTATAGTTACAGTTAACTTTATTTGGTGAATACCTTTGACAT 887

DB 781 TTATTTATGAATATAGCTATAGTTACAGTTAACTTTATTTGGTGAATACCTTTGACAT 840

QY 888 ATAAACTCTGTAACGTCAGCGGAATTTTCTTAAACTTAAATATTAAGAGCAGCTATTTT 947

DB 841 ATAAACTCTGTCATCGTACGGAATTTTCTTAAACTTAAATATTAAGAGCAGCTATTTT 900

QY 948 CAGATTTTTCGTGGCCAAAGTTTCTTCATCTACTATGCGCATTTTACTTTTATCG 1007

DB 901 AATATTTTTCGTGGCCAAAGTTTCTTCATCTACTATGCGCATTTTACTTTTATCG 960

QY 1008 TTCTAGCCTTCTAGGTACAGTTTGAACATAAAATATCAATAAAATTTGAAAGTAAATAAT 1067

DB 961 TTCTAGCCTTCTAGGTACAGTTTGAACATAAAATATCAATAAAATTTGAAAGTAAATAAT 1020

QY 1068 AGTTTTTTTTTTCATATTAATCTCGTAGGATCAATTTGTAGATCAATCTGAATAATACAA 1127

DB 1021 AG-----TTTTTTTTTTCATATTAATCTCGTAGGATCAATTTGTAGATCAATCTGAATAATACAA 1077

QY 1128 ACCATTCTGATTTTAAATCACAACCATCTCGCAAGGGGAAGTCTAT---GTGATCCGT 1184

DB 1078 ATCATCTGATTTTAAATCACAATCTATCTCGATGATGGGAACGCTCTATGGTGAATCGT 1137

QY 1185 GACAAGTGGTTGATTTATTTCTTAGTCTTAGATTGGAGTCACAACTTTTAGTGCAAAATCT 1244

DB 1138 GACAAGTGGTTGATTTATTTCTAAGTCTGGATGGAGTCACAACTTTTAGTGCAAAATCT 1197

QY 1245 ATTAAGAGAACCCCTATTGATGCAATATCTATTAAGAGAACCCCTATTTCATGCTTTAT 1304

DB 1198 ATTAAGAGAACCCCTATTGATGCAAAAGTCAATAAA--TATTTAATATCATCTTTAT 1255

QY 1305 TATTTTACGATCGGAGCATGGATATTTTACTTAATTAATAAATTTGGAAGCAATTTGAT 1364

DB 1256 TATTTTACGATCGGAGCATGGATATTTTACTTAATTAATAAATTTGGAAGCAATTTGAT 1315

QY 1365 CGACAGTCATCAAGCTTATCGTCGATCCACATTAATAAATAGCTTAGTATGGCTGCTTTT 1424

DB 1316 CGACAGTCATCAAGCTTATCGTCGATCCACATTAATAAATAGCTTAGTATGGCTGCTTTT 1375

QY 1425 AGAAGAACCAAGTGGATCATGTATAATTTAGTTTAAATATCTCTATAAATATCTATAT 1484

DB 1376 AGAAGAACCAAGTGGATCATGTATAATTTAGTTTAAATATCTCTATAAATATCTATAT 1435

QY 1485 ATACCTCTTAAACTAAATCGATCTAACACAAATATAAATCTTAGATTTCTTTAAAGAA 1544

XX Tobacco osmotin gene and non-transcribed 5' flanking sequence.
 XX Nicotiana tabacum; tobacco; osmotin; promoter; ds.
 XX Nicotiana tabacum.
 XX Key Location/Qualifiers
 XX CDS 2034..2774
 XX FT /*tag= a
 XX FT /transl_except= (pos:2574..2576,aa:Arg)
 XX
 XX US5874626-A.
 XX
 XX 23-FEB-1999.
 XX
 XX 12-JAN-1994; 94US-00180428.
 XX
 XX 20-MAY-1993; 93US-00065147.
 XX
 XX (PURD) PURDUE RES FOUND.
 XX
 XX Hasegawa PM, Bressan R;
 XX
 XX WPI; 1999-180080/15.
 XX P-PSDB; AAW94510.
 XX
 XX Tobacco osmotin gene promoter - and recombinant construct comprising
 XX foreign gene under its control.
 XX
 XX Claim 1; Fig 9A; 26pp; English.
 XX
 XX The present sequence represents the DNA sequence comprising the Nicotiana
 XX tabacum (tobacco) osmotin gene and non-transcribed 5' flanking (promoter)
 XX sequence. The present invention specifically claims a DNA fragment
 XX comprising the osmotin gene promoter sequence with no more than 100 bp of
 XX the coding sequence. Also described are methods which are useful in
 XX processes for achieving expression of a coding sequence from a foreign
 XX gene in a host cell
 XX
 XX Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;
 XX
 XX Query Match 30.0%; Score 479.2; DB 2; Length 3033;
 XX Best Local Similarity 76.9%; Pred. No. 1.4e-95;
 XX Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;
 XX
 XX 46 GGTATCTTTGTTGAAAAAATTCGAAAGACGTAGGACACATGACCTTGGTGCAC 105
 XX 2622 GGCATCTTTGTTGAAAAAATTTTGAGAAAAATAGGACCAAGGTCTTGTGTGCAAC 2563
 XX
 XX 106 AATATTGTTCTCTCCAAATGCGTACAGGATGTTACATCTCCGGGTACTTTAAAGTT 165
 XX 2562 AATATTGTTCTCTCCGAATGATGACAGGGTTATTACATCTCCGGGACCCCTAAGTT 2503
 XX
 XX 166 GACACGGGCAATTCACCAATTTATTTGCGGTGCAATGAAATGTTGTCGCAATTCCTCCAC 225
 XX 2502 CGCGGGGACATTCGCGCTTTATATTAGCCGTACAATGAATTTGCATGGCAATTCCTCCAC 2443
 XX
 XX 226 TTGGATTAGTCGGGGGGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTCOC 285
 XX 2442 TAGGTTAGTCGGGGGGAAGTCAATCGGTATTTGAATTCATCACTAAAGAAATGTCOC 2383
 XX
 XX 286 AGAAATCTAAAGTTGTTGAATCTGTCACAGCGTACTCGGTAGGGTGTGTTGTTGTC 345
 XX 2382 AGAAATCTAAAGTCAATTTGTTGTCACAGCGTATTGAGCAAGGTGTTGTTGTTGTTAC 2323
 XX
 XX 346 CCCACCGGTGCACTGACGACACCAACCAATCACCAGTCATGACCAACCTCTACACAG 405
 XX 2322 CCCACCGGTGCACTGAGGACCTCCACCAAGTCACCGGTTTGGACAGTACCCCTACACAG 2263
 XX
 XX 406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTGTAGTCCCTAGGGC 465
 XX 2262 CAGCATTTGAAGTTACAATTAGTAGCGGCCCCCATACAGTGCCTTTTAGTACCTCGTGGCG 2203

QY 466 CATCAATGACCCACATTTGGCCCCGATCGAAACGTGG-CACCGGCTTTGGGGTGGATG 524
 DB 2202 CATTGATCACCCAAAGTTTGGCTCGATCGAGACGCCGCCACCGCTATGGGTGTCGACG 2143
 QY 525 CCGCCCAACGATGATGAGCAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAG 584
 DB 2142 CCGCCCAACGATGATGAGCAGTTGTTGGGACCTCGATAGTGGCAGCATAGTGAAG 2083
 QY 585 TCACAAAAGCAAGGAGGAGAAACAAAAGAAAGATCTCAAGTAGGCCCATGTTTGTGAAA 644
 DB 2082 TCACCAAGGCAAGGAGGAGAAACAAAAGAAAGATCTCAAGTTGCCCATGTTGTTGACA 2023
 QY 645 TTTATATGTGGACAAATTTTGTGGTACT-----TTATATATAGG 685
 DB 2022 TTTTATTAACAAGTTGGGTTGTTGGATATAGTGACAAATTTGTAGTGGTTATATAGG 1963
 QY 686 GATATGGCGGCTTTTGGCACTACGATATTAATCGTATTATATAGCAATATCATACTTTG 745
 DB 1962 GGAATGGCGGCTTTTGGCACTACGATATTAATCGTATTATATAGCAATATCATACTTTG 1908
 QY 746 ACTAATTATAAACGAATATATATACAAATATGATTTGGTAAACGTTGAGGTGG-AAAAATG 804
 DB 1907 ACTA---ATRAACGGATATATCTCAAGGATGCTTTGGCAAGATGGAGGCGGCTTAAA 1851
 QY 805 TATAAGGCGGCTTAATTAATTAATTTTATGAATATAGCTATAGTACAAGTTAACT 864
 DB 1850 CATAAGGCGGCTTAATTAATTAATTTTATGAATATAG-----AAGTCAT 1803
 QY 865 TTATTGGTGATAACTTTTGACATATAAACTCTGTAACGTGAC 906
 DB 1802 TTATTGGTAAACGCTGACCTATAATCTCTGTAACGTGAC 1761
 RESULT 6
 AAQ15269/c
 ID AAQ15269 standard; cDNA; 883 BP.
 XX
 XX AC AAQ15269;
 XX
 XX DT 25-MAR-2003 (revised)
 XX DT 16-MAR-1992 (first entry)
 XX
 XX DE Osmotin-like antifungal protein.
 XX
 XX KW tobacco; osmotic tolerance; ss.
 XX
 XX OS Nicotiana tabacum.
 XX
 XX FH Key Location/Qualifiers
 XX CDS 17..757
 XX FT /*tag= a
 XX FT /note= "osmotin-like"
 XX
 XX PN EP460753-A.
 XX
 XX PD 11-DEC-1991.
 XX
 XX PF 31-MAY-1991; 91EP-00201344.
 XX
 XX PR 07-JUN-1990; 90NL-00001293.
 XX
 XX PA (MOGE-) MOGEN INT NV.
 XX
 XX PI Woloshuk CP, Melchers LS, Cornelisse BJ, Meulenhoff BJ;
 XX PI Selabuurla MB, Vandenberg PJ;
 XX
 XX DR WPI; 1991-36235/50.
 XX DR P-PSDB; AAR15660.
 XX
 XX PT New antipathogenic proteins obtd. from plants - obtd. by inducing
 XX PT resistance in plant to pathogen and pregn. of extract from plant.
 XX

PS	Claim 18; Page 17; 25pp; English.	XX	Key	Location/Qualifiers
XX		XX	CDS	17..694
CC	The full-length cDNA clone encoding antifungal protein AP20 was obtained from a lambda ZAP cDNA library prepared from tobacco mosaic virus-infected Samsum NH tobacco leaves. The library was screened with a probe for sequences homologous to the NP24 gene of tomato. One positive clone was found to contain the complete coding sequence for osmotin except for the A-T dinucleotide of the translation initiation codon. With the use of PCR, a BamHI site and an A-T dinucleotide was introduced in front of the osmotin cDNA; behind the gene a BamHI site was introduced. See also AAQ15270. (Updated on 25-MAR-2003 to correct PI field.)	XX		/tag= a
XX		XX		/note= "secretable osmotin-like protein"
XX		XX	EP460753-A.	
XX		XX	11-DEC-1991.	
XX		XX	31-MAY-1991;	91EP-00201344.
XX		XX	07-JUN-1990;	90NL-00001293.
XX		XX	(MOGE-) MOGEN INT NV.	
XX		XX	Woloshuk CP, Melchers IS, Cornelisse BJ, Meulenhoff EJ;	
PI		PI	Selabuurla MB, Vandeneize PJ;	
XX		XX	WPI; 1991-363235/50.	
DR		DR	P-PSDB; AAR15661.	
XX		XX	New antipathogenic proteins obtd. from plants - obtd. by inducing resistance in plant to pathogen and prepn. of extract from plant.	
PT		PT	Claim 18; Page 19; 25pp; English.	
XX		XX	The full-length cDNA clone encoding antifungal protein AP20 was obtained from a lambda ZAP cDNA library prepared from tobacco mosaic virus-infected Samsum NH tobacco leaves (see AAQ15269). To allow secretion of the protein into the extracellular space, a T residue was inserted between nucleotides 694 and 695 of AAQ15269. This introduces a STOP codon. The mutated cDNA thus encodes an osmotin lacking the 20 C-terminal amino acids of the wild-type osmotin and which is targeted extracellularly. (Updated on 25-MAR-2003 to correct PI field.)	
XX		XX	Sequence 884 BP; 220 A; 198 C; 205 G; 261 T; 0 U; 0 Other;	
SQ		SQ	Query Match 27.0%; Score 430.2; DB 2; Length 884;	
			Best Local Similarity 84.1%; Pred. No. 6.4e-85;	
			Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;	
QY	46 GGTATCTTTGTTTCAAAAATTTGAAAGACGTAGGACCAACATGGACCTTGGTGCAAC 105	QY	46 GGTATCTTTGTTTGAATAAATTGAAAGACGTAGGACCAACATGGACCTTGGTGCAAC 105	
DB	605 GGCATCTTTGTTTGAATAAATTGAAAGACGTAGGACCAACATGGACCTTGGTGCAAC 546	DB	605 GGCATCTTTGTTTGAATAAATTGAAAGACGTAGGACCAACATGGACCTTGGTGCAAC 546	
QY	106 AATATTGTTGTCCTCCAAATGTTGACAGGATTTACATCTCCGGTACTTTAAGTT 165	QY	106 AATATTGTTGTCCTCCAAATGTTGACAGGATTTACATCTCCGGTACTTTAAGTT 165	
DB	545 AATATTGTTGTCCTCCAAATGTTGACAGGATTTACATCTCCGGGAAACCTTAAGTT 486	DB	545 AATATTGTTGTCCTCCAAATGTTGACAGGATTTACATCTCCGGGAAACCTTAAGTT 486	
QY	166 GACCAGGGCATTTCAACATTTATATTGCGTGCAATTGAATTGTTGGCATTTCCCTCCAC 225	QY	166 GACCAGGGCATTTCAACATTTATATTGCGTGCAATTGAATTGTTGGCATTTCCCTCCAC 225	
DB	485 CGCGGGACATTCGCGGTTTATATTAGCGTACAAATGAATTGCGCATTTCCCTCCAC 426	DB	485 CGCGGGACATTCGCGGTTTATATTAGCGTACAAATGAATTGCGCATTTCCCTCCAC 426	
QY	226 TTGGATTTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCC 285	QY	226 TTGGATTTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCC 285	
DB	425 TAGGGTTAGTCGGGGGAAAGTCATCGGAATGTTGAATCCATCAACTAAGAAATGTCCC 366	DB	425 TAGGGTTAGTCGGGGGAAAGTCATCGGAATGTTGAATCCATCAACTAAGAAATGTCCC 366	
QY	286 AGAATCTAAAGTTGTTGAACCTGCTCCAGGGCTACTCGGCTAGGTTGTTGGTTTGC 345	QY	286 AGAATCTAAAGTTGTTGAACCTGCTCCAGGGCTACTCGGCTAGGTTGTTGGTTTGC 345	
DB	365 AGAATCTAAACCACTGAATGTTGTCGAAGCTATTTCAGCCAGGTGTTGGTGGTTAC 306	DB	365 AGAATCTAAACCACTGAATGTTGTCGAAGCTATTTCAGCCAGGTGTTGGTGGTTAC 306	
QY	346 CCCACCGGTGCACTGCAGGACACCAACCAATACCAAGTATGACAGCAACTCTTACCAG 405	QY	346 CCCACCGGTGCACTGCAGGACACCAACCAATACCAAGTATGACAGCAACTCTTACCAG 405	
DB	305 CCCACCGGTGCACTGCAGGACCTCCACACAGTCCACCGGTTTGGACGCTACCCCTACCAG 246	DB	305 CCCACCGGTGCACTGCAGGACCTCCACACAGTCCACCGGTTTGGACGCTACCCCTACCAG 246	
QY	406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGGCCCTTAGGGG 465	QY	406 CACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGGCCCTTAGGGG 465	
DB	245 CAGCATTTGAAGTTACAAATTAGTACGCGCCCACTACACGTGCTCATTTAGTACCTCTGTTGGG 186	DB	245 CAGCATTTGAAGTTACAAATTAGTACGCGCCCACTACACGTGCTCATTTAGTACCTCTGTTGGG 186	
QY	466 CATCAATGACCCACATTTTGGCCCGCATCGAAACGTCGG - CACCCGCTTTTCGGGGTCGATG 524	QY	466 CATCAATGACCCACATTTTGGCCCGCATCGAAACGTCGG - CACCCGCTTTTCGGGGTCGATG 524	
DB	185 CATTGATCACCCCAAGTTTGGCCCTCGATCGAGAGCGCGCCACCGCTATGTTGGTTCGACG 126	DB	185 CATTGATCACCCCAAGTTTGGCCCTCGATCGAGAGCGCGCCACCGCTATGTTGGTTCGACG 126	
RESULT 7				
ID	AAQ15270/c	ID	AAQ15270 standard; DNA; 884 BP.	
XX		XX		
XX	AAQ15270;	XX		
DT	25-MAR-2003 (revised)	DT		
DT	16-MAR-1992 (first entry)	DT		
XX		XX	Encodes C-terminally truncated osmotin-like antifungal protein.	
DE		DE	tobacco; osmotic tolerance; AP20; ss.	
XX		XX		
XX		XX	Nicotiana tabacum.	
OS		OS		


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XX SQ Sequence 1004 BP; 288 A; 200 C; 211 G; 305 T; 0 U; 0 Other;
Query Match 22.7%; Score 362.2; DB 2; Length 1004;
Best Local Similarity 77.3%; Pred. No. 6.1e-70;
Matches 466; Conservative 0; Mismatches 133; Indels 4; Gaps 2;

QY 49 ATCTTTCTTTGAAATTTGAAAGAACTAGGACACATGACCTTGGTGCAACAAT 108
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QY 109 ATCTTTCTTTGAAATTTGAAAGAACTAGGACACATGACCTTGGTGCAACAAT 168
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 546 ATCTTTCTTTGAAATTTGAAAGAACTAGGACACATGACCTTGGTGCAACAAT 487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 169 CAGGCAATTCACCAATTTATTTTGGCTGTCGATGAAATGTCGCAATTCCTCCACTTG 228
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 486 CAGGCAATTCACCAATTTATTTTGGCTGTCGATGAAATGTCGCAATTCCTCCACTTG 427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 229 GATTAGTCGGGGGAAAGTATTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCAG 288
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 426 GCTTAGTCGGGGGAAAGTATTCATCGGTATTTAAATCCATCAACTAAAGAAATGTCCAG 367
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 AATCTAAGTTGTTGAATGTTGCTGTCGATGAAATGTCGCAATTCCTCCACTTG 348
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 366 AATCTAAGTTGTTGAATGTTGCTGTCGATGAAATGTCGCAATTCCTCCACTTG 307
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 ACCGGTGCATGACGACACACCAATCACCAGTCATGCGCAACCTCTACCAAGCAC 408
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 306 ATCTTTGCAATTCAGACTTACCAATCACCAGTCATGCGCAACCTCTACCAAGCAC 247
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QY 409 CATCGAAGTTACATCCAGTACGACCCCATATACCTGCTAGTGTCCCTAGGCGCAT 468
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QY 246 CATCAAGTTGCAATTTAGTACGACCCCATATACCTGCTAGTGTCCCTAGGCGCAT 187
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QY 469 CAATGACCCCATTTGCCCCGATCGAAGTCGCGCACCGCTTC-GGGGTGATGCGG 527
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 186 AGAACCCCACTTTGACCTCGTTCGAGACGTCGCGCACCGCTTCAGGGGTTGCCGCTG 127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 528 CCCAAGCATGTATGGACAGTTGTTGGCTACCTC--GATAGTGGCAGCATAGTGAAG 584
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QY 126 CCCAGCGGTATGGGCAATTTGTTGACTTCAATACGCGGAAGCATAGTATAAG 67
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAA 644
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RESULT 10
AAC47993/c
ID AAC47993 standard; DNA; 906 BP.
XX AC AAC47993;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55872.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX SQ 25-FEB-2000; 2000EP-00301439.

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PR	11-AUG-1999;	99US-0148319P.	QY	160 TAAGTTACACAGGCGCATTCACATTTATTTGCGGTGCATTTGAATTTGTTGGCATTTCC 219	
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QY 640 TGAATTTA 648
Db 30 TTAGTTCTA 22

RESULT 11
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ID AAC47227 standard; DNA; 902 BP.
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AC AAC47227;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic pathway;
KW Promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
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PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0138847P.
PR 16-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 22-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
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PR	09-AUG-1999;	99US-0147493P.	
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PR	10-AUG-1999;	99US-0148171P.	
PR	11-AUG-1999;	99US-0148319P.	
PR	12-AUG-1999;	99US-0148341P.	
PR	13-AUG-1999;	99US-0148565P.	
PR	13-AUG-1999;	99US-0148684P.	
PR	16-AUG-1999;	99US-0149368P.	
PR	17-AUG-1999;	99US-0149175P.	
PR	18-AUG-1999;	99US-0149426P.	
PR	20-AUG-1999;	99US-0149722P.	
PR	20-AUG-1999;	99US-0149723P.	
PR	20-AUG-1999;	99US-0149929P.	
PR	23-AUG-1999;	99US-0149902P.	
PR	23-AUG-1999;	99US-0149930P.	
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PR	26-AUG-1999;	99US-0150884P.	
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PR	30-AUG-1999;	99US-0151303P.	
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PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
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PR	04-OCT-1999;	99US-0157117P.	
PR	05-OCT-1999;	99US-0157753P.	
PR	06-OCT-1999;	99US-0157865P.	
PR	07-OCT-1999;	99US-0158029P.	
PR	08-OCT-1999;	99US-0158232P.	
PR	12-OCT-1999;	99US-0158369P.	
PR	13-OCT-1999;	99US-0159293P.	
PR	13-OCT-1999;	99US-0159294P.	
PR	13-OCT-1999;	99US-0159295P.	
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PR	21-OCT-1999;	99US-0160770P.	
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PR	21-OCT-1999;	99US-0160815P.	
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PR	22-OCT-1999;	99US-0160981P.	
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PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161406P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161381P.	
PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161992P.	
PR	28-OCT-1999;	99US-0161993P.	
PR	29-OCT-1999;	99US-0162142P.	

Query Match 12.3%; Score 196.2; DB 3; Length 902;
 Best Local Similarity 61.4%; Pred. No. 2e-33;
 Matches 374; Conservative 0; Mismatches 218; Indels 17; Gaps 3;

QY	46	GGTATCTTTTTCAGAAAAATTCGAAAAGAACGTAGGACACATG-----GACCTTGGG	99
DB	615	GGCATCTCTGCTTAAAGAACTCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTCG	556
QY	100	TGCAACAATATTTGTCCTCAAAATGTGGTACAAAGATTGTTATCATCTCCGGGTACTT	159
DB	555	TACAACAGTATTTGTTCTGCTGAAATACAGTACACGGGTTGTTTCATCCACCTGGGCTC	496
QY	160	TAAATTGACCAAGGCATTCCACATTTATTTGCGTGCATTTGAATTTGTGGCATTTCC	219
DB	495	TCACACGTTTGGACATTTGCTCGTTTATTTGCTCGGTACATAGTATCCGATGGCAGTTC-	437
QY	220	CTCCACTTTGATTTAGTCGGGCGGAAAGTCATCGGTATATTAAATCCATCACTAAAGAA	279
DB	436	-----GAACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA	385
QY	280	TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAGGGGTACTCGGCTAGGTTGGTTCGTTG	339
DB	384	TATCGTAGAGTCTAAGTTGTTGAAATTTGGTTCAAAGCGTACTCAGCCAACTGTTTGGTG	325
QY	340	GTTTGCCCGCCCGGTGCATTCGACGACACCAACCAATCACCAGTATGTCACGAACTC	399
DB	324	GCTGTCCCGCCAGCTACATTTGGAGTCCACACTGCAGTCACCAAGTTTGGCATCGGCCAC	265
QY	400	TACAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATGTTAGTGCCTC	459
DB	264	GACCTGAGGAGTCAAAGTTACATTTGGTCTCTACCCCAATCCCGTCCATTTAGTGCCCG	205
QY	460	TAGGCGCATCAATGACCCACATTTGGCCCGCATCGAAACGTCGGCACCCGCTTTCCGGGGT	519
DB	204	CGCGACATCTAGCTCCATGATTTGGCAGCATCTAGACGTCCG--CCACTCCAGGGCT	147
QY	520	CGATGCGCCCAACGATGTTATGACAGTGTGTTGCGTACTCTCGATATGGCAGCATAGT	579
DB	146	TGGCGAGCCACACGGTAACTACATTTGGTTTAGGATTTCCGAATGTGGCGGCTGTGC	87
QY	580	GAAAGTCACAAAGCAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGT	639
DB	86	GGTGAGATGAGCAAAAGTCCGGAATAATGAAAGTAGAGACCAAGAGTTTGCCATTTT	27
QY	640	TGAAATTTA 648	
DB	26	TTAGTTCTA 18	
RESULT 12			
ABZ14313/c			
ID	ABZ14313 standard; DNA; 735 BP.		
XX	AC ABZ14313;		
XX	DT 21-JAN-2003 (first entry)		
XX	Arabidopsis thaliana stress regulated gene SEQ ID NO 2118.		
XX	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.		
XX	Arabidopsis thaliana.		
XX	WO200216655-A2.		
XX	28-FEB-2002.		
XX	24-AUG-2001; 2001WO-US026685.		
XX	24-AUG-2000; 2000US-0227866P.		
XX	26-JAN-2001; 2001US-0284647P.		
XX	22-JUN-2001; 2001US-0300111P.		
XX	(SCRI) SCRIPPS RES INST.		
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.		
PI	Harper JF, Krebs J, Wang X, Zhu T;		

XX WPI: 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and

XX producing plants with increased tolerance to these abiotic stresses.

XX

XX Claim 144; SEQ ID NO 2118; 577pp + Sequence Listing; English.

XX

XX The invention relates to identifying a stress condition to which a plant

XX cell has been exposed, comprising: (a) contacting nucleic acid

XX representative of expressed polynucleotides in the plant cell with an

XX array or probes representative of the plant cell genome; and (b)

XX detecting a profile of expressed polynucleotides in the plant cell

XX characteristic of a stress response. The method is useful in the

XX production of transgenic plants, cells and seeds and in producing plants

XX with increased tolerance to abiotic stress. The present sequence is that

XX of an Arabidopsis thaliana stress regulated gene (ABZ1196-ABZ17574) used

XX in methods of the invention. Note: The sequence data for this patent is

XX not represented in the printed specification but is based on sequence

XX information supplied to Derwent by the European Patent Office

XX

XX Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

XX

Query Match 12.3%; Score 195.6; DB 6; Length 735;

Best Local Similarity 62.3%; Pred. No. 2.6e-33;

Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3

QY 46 GGTATCTTTGTTTGA AAAAATTCGAAAGACGTAGACACATG-----GACCTTGGG 99

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 586 GGCATCTCTGCTTAAAGAACTCTTGAGTACTCAGTATCGCTACATGATCCTGACCGTTGC 527

QY 100 TGCACAATATTTTGTCTCTCCATATGTTGGTACAAAGATTGTTACATCTCTCGGGTACT 159

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 526 TACAACAGTATTGGTTTCGCTCGAATACAGTACACGGGTGTTTGCATCCACCTCGGGCTC 467

QY 160 TAAGTTGACAGGCATTCACATTTATTTGCGGTGCATTGAAATGTGTGCGATTCC 219

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 466 TCACACGTTTGCACATTGTCGTTTATGTCTCGGGTACATAGTATCCGATGTCAGTTTC- 408

QY 220 CTCACCTTGGATTAGTCGGGGCGAAGTCATCGGTATATAATTCATCACTAAAGAAA 279

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 407 -----GAACTAGTTGGCTAACTCCATAGTATGTTAAATCCATCGACAAGTGAGA 356

QY 280 TGTCCAGAAATCTAAGTTGTTGAAGTCTGATCGTCAAGGGGTACTCGGCTAGGGTGTGTTGGT 339

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 355 TATCGTAGAAGTCTAAGTTGTTGAATTCGGTTTCAAGCGTACTCAGCCACGTTGTTGGTG 296

QY 340 GTTTGCCCCACCGGTGCACTCGAGGACACACCAATCACAGTCACTGACGAACTCTC 399

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 295 GCTGTCCCAGCAGTACATTTGGAGTCCACACTGCACTGCAAGTTTGGCATCGGCCAC 236

QY 400 TACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCGCC 459

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 235 GACCTGAGGAGTCAGAAAGTTTACAATTTGGTCTTACCCCAAATCCGTCGCAATTTAGTCCCG 176

QY 460 TAGCGCATCATGACCCACATTTGGCCCCGATCGAAACGTCGGCACCCCGCTTTCCGGGT 519

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 175 CCGCGCATCTAGCTTCCATGATTTGGCAGCATCTAGACGTCGG--CCACTCCAGGGCT 118

QY 520 CGATGCGGCCCAACGATGTATGGACAGTTGTTGCGTACCTTCGATAGTGGCAGCATAAAGT 579

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 117 TCGCGCAGCCACACCGTGTAACTACATTTGTTTAGGATTTTCGAATGTGCGCGCTGTTCG 58

QY 580 GAAAGTCAAAAAGCAAGGGAGAAACAAAGAGATCTCAAG 625

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 57 GGTGGAGATGAGCAAAAGTCCGAAAATATGAAGTAGAGACCAAG 12

XX

RESULT 13

ABZ42096/c

ID AB242096 standard; cDNA; 735 BP.

XX ABZ42096;

Db 355 TATCGTAGAAGTCTAAGTTGTTGAATTGTTTCAAAGCGTACTCAGCCAAAGTGTGTTGGT 296
 Qy 340 GTTTCGCCCCACCGGTGACATGCGAGGACACACACATCACCAGTCAATGACGAACTC 399
 Db 295 GCTGTCCCGCAGCGATCATTTGGAGTCCACCACTGCAGTACCAGTTGGCATCGGCCAC 236
 Qy 400 TACCAGCACCATCGAAGTTACATCCAGTACGACGCCCATATACCTTGCCATGTTAGTGCCCC 459
 Db 235 GACCTGAGAGTCAAAGTTCAATTTGGTCTTACCCCAATCCGTCATTTAGTGCCCG 176
 Qy 460 TAGCGGATCATGACCCACATTTGGCCCGATCGAAACGTGCGCACCCCGTTTCGGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTCGG-CCACTCCAGGGCT 118
 Qy 520 CGATCGCCGCCCAACGATGTATGACAGTTGTTGCTGCTACCTGCTGATGTCGACGATAGT 579
 Db 117 TCGCGACGCCACACGGTGTAACTACATTTGTTTGGATTTGATGTTGGCGGTGTTGC 58
 Qy 580 GAAAGTCAAAAAGCAAGAGGGGAGAAACAAAGAGAGATCTCAAG 625
 Db 57 GGTGGAGATGAGCAAAAGTGGCGAAATATCAAAAGTAGAGACCAAG 12

RESULT 14

ADA68525/c

ID ADA68525 standard; DNA; 735 BP.

XX AC

XX AC

XX AC

XX 20-NOV-2003 (first entry)

XX Arabidopsis thaliana gene, SEQ ID 566.

XX Plant; bacterial infection; fungal infection; viral infection; ds.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to

XX pathogenic infection for conferring resistance or tolerance to a plant to

XX bacterial, fungal or viral infection by determining or detecting plant

XX gene expression.

XX Claim 6; SEQ ID NO 566; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes

XX involved in plant resistance or response to pathogenic infection. M1

XX comprises identifying a gene whose expression is significantly altered in

XX the incompatible interaction of plant gene expression relative to

XX expression of the gene in an uninfected plant, in a mutant plant that

XX does not express a gene associated with response to pathogenic infection,

XX or in a corresponding incompatible or compatible interaction. (M1) is

XX useful for conferring resistance to resistance or tolerance to a plant to

XX bacterial, fungal or viral infection. The present sequence was used to

XX illustrate the invention.

XX Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

XX Query Match 12.3%; Score 195.6; DB 7; Length 735;

Best Local Similarity 62.3%; Pred. No. 2.6e-33;
 Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;

Qy 46 GGTATCTTTGTTTGAATAAATTGGAAGAGAGTGGAGCCACATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGTACATGATCCCTGACCGTTTCG 527
 Qy 100 TCGAACATATTTGTTGCTCCTCAATGTGGTACAGAGATTGTACATCTCGGGTACTT 159
 Db 526 TACAACAGATTTGGTTCGTTCTGAAATACAGTACACGGGTTGTTGCATCCCTCGGGGTC 467
 Qy 160 TAAAGTTGACGAGGCAATTCACCATTTATATTGCGTCAATTTGAATTTGTGGCAATTTCC 219
 Db 466 TCACACACGTTGGACATTTGTCGGTATATGTTCTCGGTACATAGTATCCGATGGCAGTTC- 408
 Qy 220 CTCCTACTTTGGATTTAGTTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACAAAGAA 279
 Db 407 -----GAACCTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAAAGTGAGA 356
 Qy 280 TGTCCGAGAAATCTAAGTTGTTGAACTGCTCCAGGGCTACTCGGCTAGGTTGTTGGTG 339
 Db 355 TATCGTAGAGTCTAAGTTGTTGTTGTTTCAAGGCTACTCAGCCAACTGTTTGGTG 296
 Qy 340 GTTTCGCCCAACCGGTGCACTGCGAGGACACCAATCAATCAATCAATCAATCAATCAATCAAT 399
 Db 295 GCTGTCCCGCAGCCAGTACATTTGGAGTCCACACTGCAGTCCAGTTCGATTCGCGCAC 236
 Qy 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCTGCTAGTGGCCCC 459
 Db 235 GACCTGAGGAGTCAAAGTTTCAATTTGCTTACCCCAATCCGTTGCTGCTAGTGGCCCC 176
 Qy 460 TAGCGCATCAATGACCCACACATTTGGCCCCCATCGAAACGTCGCGCACCCGCTTTCCGGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTCGG--CCACTCCAGGGCT 118
 Qy 520 CGATGCGCCCCCAACGATGTATGACAGATTGTTGCTGCTACCTCGATAGTGGCAGATAGT 579
 Db 117 TCGCGACGCCACACCGGTGTAATACATTTGTTTGGATTTTGAATTTGCGGGCTGTTGC 58
 Qy 580 GAAAGTCAAAAAGCAAGAGGGGAGAAACAAAGAGAGATCTCAAG 625
 Db 57 GGTGGAGATGAGCAAAAGTGGCGAAATATCAAAAGTAGAGACCAAG 12

RESULT 15

ABN98566/c

ID ABN98566 standard; DNA; 950 BP.

XX AC

XX AC

XX AC

XX 01-AUG-2002 (first entry)

XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 334.

XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;

XX disease; crop; thale cress; tolerance factor; insect; pathogen;

XX nutrition; ds.

XX Arabidopsis thaliana.

XX US2002023281-A1.

XX 21-FEB-2002.

XX 26-JAN-2001; 2001US-00770445.

XX 27-JAN-2000; 2000US-0178472P.

XX (GORL/) GORLACH J.

XX (ANY/) AN Y.

XX (HAMI/) HAMILTON C M.

XX (PRIC/) PRICE J L.

XX (RAIN/) RAINES T M.

PA (YUYX//) YU Y.
 PA (NAME//) RAMEAKA J G.
 PA (PAGE//) PAGE A.
 PA (MATH//) MATHW A V.
 PA (LEDF//) LEDFORD B L.
 PA (WOES//) WOESSNER J P.
 PA (HAAS//) HAAS W D.
 PA (GARC//) GARCIA C A.
 PA (KRIC//) KRICKER M.
 PA (SLAT//) SLATER T.
 PA (DAVI//) DAVIS K R.
 PA (ALLE//) ALLEN K.
 PA (HOFF//) HOFFMAN N.
 PA (HURB//) HURBAN P.
 XX
 PI Grolach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI; 2002-403163/43.
 XX
 PT New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of protein.
 XX
 PS Claim 1; SEQ ID NO 334; 49pp + Sequence Listing; English.
 XX
 CC The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful for
 CC enhancing or inhibiting production of a biosynthetic product in a plant.
 CC (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=999909770445
 XX
 SQ Sequence 950 BP; 261 A; 225 C; 213 G; 251 T; 0 U; 0 Other;
 Query Match 12.3%; Score 195.6; DB 6; Length 950;
 Best Local Similarity 62.3%; Pred. No. 2.8e-33;
 Matches 365; Conservative 0; Mismatches 204; Indels 17; Gaps 3;
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 QY 46 GGATCTCTGTTGTAAGAAATGGAAAGAACGTAGGACCAATG-----GACCTGGG 99
 DB 594 GGCATCTCTGTTGTAAGAAATCTTGAGTACTGCTATCGTACATGATCCCTGACCGTTCG 535

QY 100 TGCACAAATATTGTTGTCCTCCAAATGTCGGTCAAGGATTGTTACATCTCCGGGTACTT 159
 DB 534 TACACAGATTATTGGTTTCGTCTGAAATACAGTACACGGGTTGTTGCATCCACCTCGGGCTC 475
 QY 160 TAAAGTTGACACAGGGCAATCCACCATTTATATTTGCGGTGCAATGGAATTGTTGGCATTTCC 219
 DB 474 TCACACAGTTTGGACATTTGTCGTTTATGTCGCGTACATAGTATCCCATGGCAGTTTC- 416
 QY 220 CTCCACTTGGATTAGTCGGGGCGCAAGTATCATCGGTATATTAATCCATCAACTAAAGAAA 279
 DB 415 -----GAACTAGTTGGGCTAAATCTCATAGGTATGTTAAATCCATCGACAAGTGAGA 364
 QY 280 TGTCCCAAGAAATCTAAGTTGTTGAACTGTCCTCAAGCGGTACTCGCTAGGTTGTTGGTG 339
 DB 363 TATCGTAGAAGTCTAAGTTGTTGAAATGTTTCAAGCGGTACTCAGCCAACGTGTTTGGTG 304
 QY 340 GTTTGCCCCCAACCGGTGCATCGCAGGACACCAACCAATCACCAGTTCATGCACGAACTTC 399
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 QY 400 TACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATACCTGCGCATCGTAGTGCCTCC 459
 DB 243 GACCTGAGGAGTCAAAAGTTTACAAATTTGGTCTCTACCCCAAAATCGTGCCATTTTAGTGCCG 184
 QY 460 TAGGCGCATCAATGACCCCAATTTGGCCCGGATCGAAACGTGCGCACCCGCTTTTCGGGGT 519
 DB 183 CCGCAGCATCTAGCTCCCATGATTTGGCCAGCATCTAGAGCTCGG--CCACCTCCAGGGCT 126
 QY 520 CGATGCGGCCCAACGATGATGTCGACAGTTGTTGGTACCTCGATGAGTGGCAGCATAAAT 579
 DB 125 TGGCGCAGCCACACGGGTGTAACACTACATGTTGTTAGGATTCGAATGTGGCGGCTGTTCG 66
 QY 580 GAAAGTTCACAAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 625
 DB 65 GGTGAGATGACCAAAAGTGGCGGAAATATGAAAGTAGAGAGCAAG 20

Search completed: August 18, 2004, 07:59:05
 Job time : 578.148 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 06:27:01 ; Search time 122.848 Seconds
(without alignments)
7205.239 Million cell updates/sec

Title: US-10-051-307-1
Perfect score: 1595
Sequence: 1 gtaatacagctactatagg.....tggtagagttggtgtcttc 1595

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	430.2	27.0	883	1 US-07-828-798C-4	Sequence 4, Appli
C 3	430.2	27.0	883	2 US-08-315-868A-4	Sequence 4, Appli
C 4	430.2	27.0	883	3 US-08-495-819B-4	Sequence 4, Appli
C 5	430.2	27.0	884	1 US-07-828-798C-5	Sequence 5, Appli
C 6	430.2	27.0	884	2 US-08-315-868A-5	Sequence 5, Appli
C 7	430.2	27.0	884	3 US-08-495-819B-5	Sequence 4, Appli
C 8	170.4	10.7	875	4 US-09-589-733C-4	Sequence 4, Appli
C 9	155.2	9.7	900	1 US-08-181-271A-4	Sequence 4, Appli
C 10	155.2	9.7	900	1 US-08-449-315-4	Sequence 4, Appli
C 11	155.2	9.7	900	1 US-08-444-803-4	Sequence 4, Appli
C 12	155.2	9.7	900	1 US-08-449-043-4	Sequence 4, Appli
C 13	155.2	9.7	900	1 US-08-456-265A-4	Sequence 4, Appli
C 14	155.2	9.7	900	1 US-08-455-416-4	Sequence 4, Appli
C 15	155.2	9.7	900	1 US-08-455-244-4	Sequence 4, Appli
C 16	155.2	9.7	900	1 US-08-454-876-4	Sequence 4, Appli
C 17	155.2	9.7	900	2 US-08-457-364-4	Sequence 4, Appli
C 18	155.2	9.7	900	2 US-08-456-262-4	Sequence 4, Appli
C 19	155.2	9.7	900	2 US-08-456-240-4	Sequence 4, Appli
C 20	155.2	9.7	900	2 US-08-455-736-4	Sequence 4, Appli
C 21	155.2	9.7	900	2 US-08-971-217-4	Sequence 4, Appli
C 22	155.2	9.7	900	3 US-09-350-600-4	Sequence 4, Appli
C 23	155.2	9.7	900	4 US-09-906-234-4	Sequence 4, Appli
C 24	149	9.3	910	4 US-09-685-232-1	Sequence 4, Appli
C 25	106.4	6.7	894	1 US-08-178-708-7	Sequence 7, Appli
C 26	106.4	6.7	894	1 US-08-457-552-7	Sequence 7, Appli
C 27	106.4	6.7	894	1 US-08-456-430-7	Sequence 7, Appli

C 28	106.4	6.7	894	2 US-08-994-418-7	Sequence 7, Appli
C 29	106.4	6.7	894	5 PCI-US95-00432-7	Sequence 7, Appli
C 30	97.4	6.1	1309	6 5221624-4	Patent No. 5221624
C 31	90.6	5.7	621	4 US-09-224-514A-1	Sequence 1, Appli
C 32	90.6	5.7	621	6 5221624-31	Patent No. 5221624
C 33	89	5.6	621	4 US-09-224-514A-9	Sequence 9, Appli
C 34	86.2	5.4	624	2 US-08-426-598B-3	Sequence 3, Appli
C 35	78.4	4.9	624	2 US-08-426-598B-1	Sequence 1, Appli
C 36	73.2	4.6	2051	1 US-08-482-037A-2	Sequence 28, Appli
C 37	64.6	4.1	230	4 US-09-589-733C-28	Sequence 1, Appli
C 38	60.8	3.8	640681	4 US-09-790-988-1	Patent No. 5231168
C 39	59	3.7	3095	6 5231168-1	Sequence 5, Appli
C 40	52.2	3.3	1924	4 US-09-424-283-5	Sequence 14, Appli
C 41	52	3.3	6113	4 US-10-204-708-14	Sequence 38, Appli
C 42	49.8	3.1	288	4 US-09-598-401C-38	Sequence 1, Appli
C 43	49.6	3.1	6152	3 US-08-973-462-1	Sequence 25, Appli
C 44	49.6	3.1	6593	4 US-10-204-708-25	Sequence 13, Appli
C 45	49	3.1	19124	2 US-08-487-826B-13	

ALIGNMENTS

RESULT 1
US-08-482-037A-1/c
; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Osmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas O. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,037A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,243
FILING DATE: June 7, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/180,428
FILING DATE: January 12, 1994
APPLICATION NUMBER: 08/065,147
FILING DATE: May 20, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas O. Henry
REGISTRATION NUMBER: 28,309
REFERENCE/DOCKET NUMBER: 7024-8/PUR16ICPDIVII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 634-3456
TELEFAX: (317) 637-7561

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 bases
TYPE: Nucleotide/Amino Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA
US-08-482-037A-1

Query Match 30.0%; Score 479.2; DB 1; Length 3033;

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Best Local Similarity 76.9%; Pred. No. 1.2e-101;
Matches 678; Conservative 0; Mismatches 163; Indels 41; Gaps 6;
QY 46 GGTATCTTTGTTGAAAGAAATTTGAAAGAAAGCGTAGGACACATGACCTTGGTGGCAAC 105
Db 2622 GGCATCTTTGTTGAAAGAAATTTGAGAGAAATGTAGGACACACAGGTCTTGTGTGCAAC 2563
QY 106 AATATTGTTGCTCCCAATGTGTACAGAGATGTACATCTCCGGGTACTTTAAGTT 165
Db 2562 AATATTGTTGCTCCCAATGTGTACAGAGATGTACATCTCCGGGTACTTTAAGTT 2503
QY 166 GACCAGGCGCATTCACCATTTATATTGCGCGTCAATGAAATGTGTGCGCATTTCCCTCCAC 225
Db 2502 CGCGGGGACATTCGCGCTTTATATTAGCGGTACAAATGAATGCGATGCAATTCCTCCAC 2443
QY 226 TTGGATTAGTCGGGGGAAAGTGTATCGGTATATTAATTCATCACTAAAGAAATGTCCC 285
Db 2442 TAGGGTTAGTCGGGGGAAAGTGTATCGGTATATTAATTCATCACTAAAGAAATGTCCC 2383
QY 286 AGAATCTAAGTTGTTGAACTGGTCCCAAGCGTACTCGGTAGGTGTTGGTGGTTTGC 345
Db 2382 AGAATCTAAGTTGTTGAACTGGTCCCAAGCGTACTCGGTAGGTGTTGGTGGTTTAC 2323
QY 346 CCCACCGGTGTCATGCGAGGACACCAACCAATCAAGTATGCGAGAACCTTCTACCAG 405
Db 2322 CCCACCGGTGTCATGCGAGGACACCAACCAATCAAGTATGCGAGAACCTTCTACCAG 2263
QY 406 CACCATCGAGTTACATCCAGTACGACCCCATATACCTGCGTATGTCGAGAACCTTCTAGGCG 465
Db 2262 CAGCATTAAGTTACATCCAGTACGACCCCATATACCTGCGTATGTCGAGAACCTTCTAGGCG 2203
QY 466 CATCAATGACCCACATTTGGCCCGCATGCAAGCGTGG-CACCGCTTTTCGGGGTCCAGT 524
Db 2202 CATGATCACCAAGTTTGGCTCGATCGAGACGCGCGCCACCGCTATGCGTGTGACG 2143
QY 525 CCGCCCAACGATGTATGGACAGTTGTTGGTACCTGATAGTGGCGCATAGTGAAG 584
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QY 645 TTTATATGTGACAAATATTTTGGTACT-----TTATATATAG 685
Db 2022 TTTTATTAACAGTTGGTTGTTGGTATAGTACAAATGTTTAGTGGTTTATATAG 1963
QY 686 GATATGGCGCTTTTGGCAGTACGATTAATTAATCGTATATATAGCAATATCATCTTTG 745
Db 1962 GGAATGGCGCTTTTGGTACTATGATATTAATC-----ATTAATATTAATTAACATTG 1908
QY 746 ACTAATTATAACGAAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
Db 1907 ACTA---ATAACGGAATATCTCAAGATGCTTTGGCAAGATGAGGCGGCGCTTAA 1851
QY 805 TATAGAGCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 864
Db 1850 CATAGAGCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1803
QY 865 TTATTGTTGATTAATCTTTGACATATAAATCTCTGAACGTGAC 906
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RESULT 2

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US-07-828-798C-4/c
; Sequence 4, Application US/07828798C
; Patent No. 5389609
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.

```

```

; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Pary
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828.798C
; FILING DATE: 06-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-07-828-798C-4

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Query Match 27.0%; Score 430.2; DB 1; Length 883;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;
Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;
QY 46 GGTATCTTTGTTGAAAGAAATTTGAAAGAAAGCGTAGGACACATGCGACCTTGGGTGCAAC 105
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QY 106 AATATTGTTGCTCCCAATGTGTACAGAGATGTGTATCATCTCCGGGTACTTTAAGTT 165
Db 545 AATATTGTTGCTCCCAATGTGTACAGAGATGTGTATCATCTCCGGGTACTTTAAGTT 486
QY 166 GACCAGGCGCATTCACCATTTATATTGCGCGTCAATGAAATGTGTGCGCATTTCCCTCCAC 225
Db 485 CGCGGGGACATTCGCGCTTTATATTAGCCGTACAAATGAATGCGATGCGATTTCCCTCCAC 426
QY 226 TTGGATTAGTCGGGGGAAAGTGTATCGGTATATTAATTCATCACTAAAGAAATGTCCC 285
Db 425 TAGGGTTAGTCGGGGGAAAGTGTATCGGTATATTAATTCATCACTAAAGAAATGTCCC 366
QY 286 AGAATCTAAGTTGTTGAACTGGTCCCAAGCGTACTCGGTAGGTGTTGGTGGTTTGC 345
Db 365 AGAATCTAAGTTGTTGAACTGGTCCCAAGCGTACTCGGTAGGTGTTGGTGGTTTAC 306
QY 346 CCCACCGGTGTCATGCGAGGACACCAACCAATCAAGTATGCGAGAACCTTCTACCAG 405
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/315,868
  FILING DATE: 30-SEPT-94
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/828,798
  FILING DATE: 06-APRIL-92
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/NL91/00089
  FILING DATE: 31-05-91
ATTORNEY/AGENT INFORMATION:
  NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-010255-1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 708-1800
  TELEFAX: (212) 246-8959
  TELEX: 233288
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  LENGTH: 883
  TYPE: Nucleotide
  STRANDEDNESS: Double
  TOPOLOGY: Linear
  MOLECULE TYPE: cDNA
  ORIGINAL SOURCE:
  ORGANISM: Nicotiana tabacum
US-08-495-819B-4

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Query Match      27.0%; Score 430.2; DB 3; Length 883;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;
Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAGAAAAATGTAGGACCAACAGGTGCTTGTGTGCAAC 546
QY 106 AATATTGTTGCTCCCAAAATGTGTAAGGATTTACATCTCTCCGGGTACTTTTAAGTT 165
DB 545 AATATTGTTGCTCCCAAAATGTGTAAGGATTTACATCTCTCCGGGTACTTTTAAGTT 486
QY 166 GACCAAGGCATTCACCAATTTATTTGCGGTGCAATGAATTTGTCGCAATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGGTGCAATGAATTTGTCGCAATTTCCCTCCAC 426
QY 226 TTGATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCC 285
DB 425 TAGGTTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCC 366
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DB 365 AGAAATCTAAGTTGTTGAATGTTGCTCCAAAGGCTACTCGGTAGGGTGTGTTGGTTTC 306
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DB 305 CCCACCGGTGCTAGTCAGGACCAACCAATCACTACCAAGTCACTGACGACCTCTACCCAG 246
QY 406 CACCATGAAGTTACATCCAGTACGACCCCATATPACCTGCGCATCTAGTGCCTTACGGCG 465
DB 245 CAGCATGAAGTTACATCCAGTACGACCCCATATPACCTGCGCATCTAGTGCCTTACGGCG 196
QY 466 CATCAATGACCCCATTTGGCCCGGANTCGAAACGTTCGG- CACCGCTTTCGGGGTGCATG 524
DB 185 CATGATCACCAAGTTGGCCCGGANTCGAAACGTTCGG- CACCGCTTTCGGGGTGCATG 126
QY 525 CCGCCCAAAACCATGTATGACGAGTGTGTCGTACTCGATAGTGGGACGATAAGTGAAG 584
DB 125 CCGCCCAAAACCATGTATGACGAGTGTGTCGTACTCGATAGTGGGACGATAAGTGAAG 66
QY 585 TCACAAAGCAAGGAGGAGAAACAAAGAAATCTCAAGTAGCCCATGT 635
DB 65 TCACAAAGCAAGGAGGAGAAACAAAGAAATCTCAAGTAGCCCATGT 15

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RESULT 5
US-07-828-798C-5/c
Sequence 5, Application US/07828798C
Patent No. 5389609
GENERAL INFORMATION:
  APPLICANT: Woloshuk, Charles P.
  APPLICANT: Melchers, Leo S.
  APPLICANT: Cornelissen, Bernardus J. C.
  APPLICANT: Meulenhoff, Elisabeth J. S.
  APPLICANT: Sela-Buurlage, Marianne B.
  APPLICANT: Van Den Elzen, Petrus J. M.
TITLE OF INVENTION: Antifungal Preparations, Process for
TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
TITLE OF INVENTION: Decreased Susceptibility to Fungi
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Ladas & Parry
  STREET: 26 West 61st Street
  CITY: New York
  STATE: New York
  COUNTRY: USA
  ZIP: 10023
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
  COMPUTER: IBM PC/XT/AT or compatibles
  OPERATING SYSTEM: DOS
  SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/828,798C
  FILING DATE: 06-APR-1992
  CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/NL91/00089
  FILING DATE: 31-05-91
  ATTORNEY/AGENT INFORMATION:
  NAME: Mass, Clifford J.
  REGISTRATION NUMBER: 30086
  REFERENCE/DOCKET NUMBER: U-8622-6
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 708-1800
  TELEFAX: (212) 246-8959
  TELEX: 233288
  INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 884
  TYPE: Nucleotide
  STRANDEDNESS: Double
  TOPOLOGY: Linear
  MOLECULE TYPE: cDNA
  ORIGINAL SOURCE:
  ORGANISM: Nicotiana tabacum
US-07-828-798C-5

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Query Match      27.0%; Score 430.2; DB 1; Length 884;
Best Local Similarity 84.1%; Pred. No. 1.8e-90;
Matches 497; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAGAAAAATGTAGGACCAACAGGTGCTTGTGTGCAAC 546
QY 106 AATATTGTTGCTCCCAAAATGTGTAAGGATTTACATCTCTCCGGGTACTTTTAAGTT 165
DB 545 AATATTGTTGCTCCCAAAATGTGTAAGGATTTACATCTCTCCGGGTACTTTTAAGTT 486
QY 166 GACCAAGGCATTCACCAATTTATTTGCGGTGCAATGAATTTGTCGCAATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGGTGCAATGAATTTGTCGCAATTTCCCTCCAC 426
QY 226 TTGATTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCC 285
DB 425 TAGGTTAGTCGGGGCGAAGTCAATCGGTATATTAAATCCATCACTAAAGAAATGTCCC 366

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Qy	286	AGAAATCTTAAGTTGTTGAACCTCGTCCAAAGCGGTACTCGCTAGGGTGTGTTGGTGGTTGC	345
Db	365	AGAAATCTAAACCCACTGAATTGCTCCAAAGCGGTATTCAGCCAAAGTGTTTGGTGGTTTAC	306
Qy	346	CCCAACCGGTGCACCTGCAGGACACACACCAATCACCAGTCATCCAGCAACCACTCTACCAG	405
Db	305	CCCAACCGGTGCACCTGTAGGACTCCACCACAGTCACCGSTTTGSCAGTACCCCTACCAG	246
Qy	406	CACCATCGAAGTTACATCCAGTACAGACCCCATATACCTGCCATCGTAGTCGCCCTTAGGCG	465
Db	245	CAGCATTTGAAGTTTACAAATTAGTACGGCCCCCATACACGTGCCAATTTTAGTACTCTCGTGGCG	186
Qy	466	CATCAATGATGCCACATTTTGGCCCCCGATCGAAACGCTCG - CACCCGCTTTTCGGGGTGCATG	524
Db	185	CATTGATCACCCAAAGTTTGGCCCTCGATCGAGACGCGGCCACACCGCTATGGGTGTCGACG	126
Qy	525	CGSCCCAAACGATGATGACAGTAGTTGTTGGCTACTCGTAGTGGCAGCATAGTGAAG	584
Db	125	CGGCCCAACCGGTGTACGCAAGTTGTTTTCGACCTCGTAGTGGCAGCATAGTATAAG	66
Qy	585	TCAAAAGACAGAGGGGAGAAAAAATAAGAGATCTCAAGTAGCCCATCT	635
Db	65	TACCAAGGCAAGGAGGAGAAAAAATAAGAGATCTCAAGTTGCCCATCT	15

RESULT 6

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US-08-315-868A-5/c
; Sequence 5, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Meichers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Eizen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
;

```

/	TYPE:	Nucleotide			
/	STRANDEDNESS:	Double			
/	TOPOLOGY:	Linear			
/	MOLECULE TYPE:	cdna			
/	ORIGINAL SOURCE:				
/	ORGANISM:	Nicotiana tabacum			
US-08-315-868A-5					
Query Match		27.0%;	Score 430.2;	DB 2;	Length 884;
Best Local Similarity		84.1%;	Pred. No. 1.9e-90;		
Matches 497;		Conservative 0;	Mismatches 93;	Indels 1;	Gaps 1;
Qy	46	GGTATCTTTCTTTGAAAAAATTCGAAAGAACCTTAGACCCACATGCACCTTGCGTGC AAC	105		
Dd	605	GGCATCTTTGTGTAATAATTTTGAGAAAANTGTAGCACCA CAAAGTCTCTTGTGTGC AAC	546		
Qy	106	AATATTGTTGTCCTCCA AATGTGGTTCARAGATTTGTATCATCTCCGGGPACTTTTAAGTT	165		
Dd	545	AATATTGTTGTCCTCCGA ATGTAGTACAAGGGTTATTACATCTCCGGGA ACCTTAAGTT	486		
Qy	166	GACCAGGGCATTCCACATTTTATATTGCCGTGCATTGAATGTGTGCGCATTTCCCCTCCAC	225		
Dd	485	C GCGGGGACATTCGCGGTTTTATATTAGACGTACATGAATGCATGSCATTTCCCTCCAC	426		
Qy	226	TTCGATAGTCGGGGCGA AGTCATCGGTATATTAATTCATCAA TAAAGA AATGTCCC	285		
Dd	425	TAGGGTTAGTCGGGGCGA AGTCATCGGAATGTGAATCCATCAACTAAAGA AATGTCCC	366		
Qy	286	AGAAATCTAAGTTGTTGAA CTGGTCCAAAGCGCTACTCGGCTAGGNGTTTGGTGGTTGC	345		
Dd	365	AGAAATCTAAACCACTGA NTTGGTCCAAAGCTATTCCACCAAGGHTTTGGTGGTTTAC	306		
Qy	346	CCACCCGGTGC ACTCGAAGACACCA CCAATCACCACTCATGCACGAACCTCTACCA G	405		
Dd	305	CCACCCGGTGC ACTGTAGGACTTCCACCA CAGTCACCGGTTTGGCACGTACCCCTACCAG	246		
Qy	406	CACCATCGAAGTTACATCCAGTACGACCCCA TATACCTGCCATCGTAGTGC CCCTAGGG	465		
Dd	245	CACATGAA GTTACAA TTAGTACGGCCCCCA TACAGTGCCATTTTAGTACCTCTGTGGCG	186		
Qy	466	CATCAATGACCCCA CATTTGGCCCCGATCGAAACGTGG -CACCCGCTTTTCGGGGTCGATG	524		
Dd	185	CATTGATCACCCCAAGTTTGG CCTCGATCGAGACCGCGGCCA CGGCTATGGGTGTCGACG	126		
Qy	525	CCGCCCAACGATGTATGACAGTGTCTTGGTACCTCCTGATAGTGGCAGCATTAAGTGAAG	584		
Dd	125	CCGCCCAACG GTGTACGACAGTGTGTTTCGACCTCGATATGTGGCAGCATTAAGTATAAG	66		
Qy	585	TCAAAAAGCAAGAGGGGAAAAACAAAAGAAGATCTCAAGTAGCCCATGT	635		
Dd	65	TCACCAAGCAAGAGGAGAAAAACAAAAGAAGATCTCAAGTTGCCCATGT	15		

RESULT 7

US-08-495-819B-5/c
 ; Sequence 5, Application US/08495819B
 ; Patent No. 6087161
 ; GENERAL INFORMATION:
 ; APPLICANT: Woloshuk, Charles P.
 ; APPLICANT: Melchers, Leo S.
 ; APPLICANT: Cornelissen, Bernardus J. C.
 ; APPLICANT: Cornelioff, Elisabeth J. S.
 ; APPLICANT: Sela-Buurlage, Marianne B.
 ; APPLICANT: Van Den Elzen, Petrus J. M.
 ; TITLE OF INVENTION: Antifungal Preparations, Process for
 ; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
 ; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ladas & Parry
 ; STREET: 26 West 61st Street
 ; CITY: New York
 ; STATE: New York

```

185  CATTGATCACCAAGTTTGGCTCGATCGAGACCGCCGACCGCCTATGGGTGTGACG 584
525  CGGCCCAACAGTGTATCGACAGTGTTCCTACTCGATAGTGGCAGCATAAAGTGAAG 584
125  CGGCCCAACCGGTGTACGACAGTGTTCGAGCTCGATAGTGGCAGCATAAAGTATAAG 66
585  TCACAAAGCAAGAGGAGGAGAAAAACAAAGAGATCTCAAGTAGCCCCATGT 635
65  TCACCAAGCAAGGAGGAAGAAAAACAAAGAGATCTCAAGTTGCCCATGT 15

RESULT 8
US-09-589-733C-4/c
; Sequence 4, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crascha, Oswald R.
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-09-589-733C-4

```

Query Match	10.7%;	Score 170.4;	DB 4;	Length 875;
Best Local Similarity	59.7%;	Pred. No. 2.2e-30;		
Matches 325;	Conservative 0;	Mismatches 211;	Indels 8;	Gaps 2;
Qy	49	ATCTTTGTTTCAGAAAAATTCGAAAAAGAACTAGACACACATGGACCTTTGGGTGCAACAAT	108	
Db	577	ATCTGGTCTTGAAAAACCTTGATAATCAGTTGGTCCCAAAATTCAGAGTTGCAACAAT	518	
Qy	109	ATTGTGTGCTCCAAATGTGGTCAAGGATGTGTAATCTCTCGGGTACTTTTAAGTTGAC	168	
Db	517	ACTGATCAGTTTGTACACGGTGCAAGGGTATTGACCGCGCAGGAGCCGTAACTCAC	458	
Qy	169	CAGGSCATTACCAATTTATTTGCGGTGCAATGGAATTGTGTGGCAATTCCTCTCCACTTG	228	
Db	457	CAGGACCTGGCCATTGATATCCGAGTACATGAGATACCCGGGTGCACCC-----AT	404	
Qy	229	GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAGAAATGTCGCCAGA	288	
Db	403	TAGAATTCGGTCTAAACACCAATCGGCACATTGAAATCCGTCCAAGAGAAATGTCAAGA	344	
Qy	289	ATCTTAAGTCTTCAACTGGTCCAAAGCGTACTCGGTAGGGTGTGTTGGTGTGTTTGGCCCC	348	
Db	343	AATCAAGATTTGTGAATGGTTTAAAGCGTATCTGGGCCAATGTGTGGTGGGTGACCAT	284	
Qy	349	ACCCGGTGCATGCAGGACACCAACAATCACCAATGACAGATNGACGAACTCTTACAGCAC	408	
Db	283	AGTTTTTGCAATTCGAGGAGACCGTTGCAATCACCGGTCTTGACACCTGCTCGCCCCAGAAC	224	
Qy	409	CATCGAAGTTCATCCAGTACGACCCCATATATCTTCCATCTGAGTGGCCCTTAGSCGCAT	468	
Db	223	CATCAAAATTTGCAATTTGGTTTCGGGGCCATATACGGGTCTCTGCTGTGCAGCTGCAGCG	164	
Qy	469	CAATGACCCCAATTTGGCCCCCGATCGAAACGTCGGACCCCGTTTCGGGGTTCGATGCGCG	528	
Db	163	TTAAAGACAGGTTTGGCTTGAGTTAAGTTGTTCGGCGGCCAC--CAGGCACCGCACCCAGC	106	

QY 529 CCAACGATGTATGACAGTGTTCGCTACCTCGTAGTGGCAGCATAGTGAAGTCAAC 588
 Db |||||
 105 CCAACGGTGTATGACAGTGTTCGCTACCTCGTAGTGGCAGCATAGTGAAGTCAAC 46
 QY 589 AAAA 592
 Db |||||
 45 AAGA 42

RESULT 9

US-08-181-271A-4/C
 ; Sequence 4, Application US/08181271A
 ; Patent No. 5614395
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/181,271A
 ; FILING DATE: 13-JAN-94
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/578,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA: US 07/848,506
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-181-271A-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTGTTGAAAAAATCGAAAAAGAGTAGGACACAT-----GGACCTTGGG 99
 Db |||||
 607 GGCATCTTTCCCTAAAAAATCTCGAATATCAGTAGGCCACATGATCCAGGCCCATTTG 548
 QY 100 TGCACAAATATTGTTCTCTCCAAATGTGTTACAGGATTGTACATCTCCGGGTACTTT 159
 Db |||||
 547 TACACAAATATTGTTCTCTCCAAATGTGTTACAGGATTGTACATCTCCGGGTACTTT 488
 QY 160 TAAGTTGACGAGGCAATCCACATTTATATTTGCGGTGCATTGAATTGTGTCGATTTCC 219
 Db |||||
 487 TCACCTGTCTGGGCAATTTGTTGTTAATAGGTGCTGTGCACTCTGAGATTACACAT 432
 QY 220 CTCCTCTGATAGTCGGGGGAAAGTCATCGGTATATTAATCAATCACTAAAGAAA 279
 Db |||||
 431 -----CTCCATTTGGTGGGCTGAATTCATGGGATGTTAAATCCATCAACAGAGAGA 377
 QY 280 TGTCCAGAAATCTAAGTTGTTGAATCTGTCAGGCGTACTCGGCTAGGGTGTGGTG 339
 Db |||||
 376 TGTCCAGAAAGTC---CTGATTGGGTGATTAAGTGAATTCAGCTAAGGTGTAGGTG 320
 QY 340 GTTTGCCCCACCCGGTGCATCTCAGGACACCAACCAATCACCAGTCATGCACGACCTC 399
 Db |||||
 319 CTTTTCATAGCTTTGACACTCAATCCCGTTACAGTCTCCAGTCTCACAATACCTC 260
 QY 400 TACCAGCACCATCGAAGTTACATCCAGTAGACCCCATATACCTGCCATCGTAGTGCCTC 459
 Db |||||
 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAATTCGAGCCTGAGCTGTTCTG 200
 QY 460 TAGGGGCATCAATGACCCACATTTGGCCCGGATCGAAACGTCGGACCCCGCTTCGGGGT 519
 Db |||||
 199 GGTTCACATTAATGCTCCAGATTGGCTGAGTCCAGCGCGCTGCTCCACCT--GGAGA 142
 QY 520 CGATCGCGCCCAACGATGTATGGACAGTTGTTGGTACCTCGATAGTGGGACGACATAAGT 579

141 GCGCGCGCCGAGACTGTGTAGTGCATTTGTTGACAATGTCAAAAGTGGCAGCATGAGT 82

580 GAAAGTCACAAA 591

81 AACAGTACAAA 70

RESULT 10

US-08-449-315-4/c

; Sequence 4, Application US/08449315

; Patent No. 5650505

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Melms, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Meyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,315

; FILING DATE: 24-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 900 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-449-315-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTGTTGAAAAAATTGGAAAAAGACGTAGGACCCACAT-----CGACCTTGGG 99

Db 607 GCATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548

QY 100 TCGAACAAATATTTGTTGCTCTCCAAATGTGGTACAGGATTTGTTACATCTCTCGGGTACTT 159

Db 547 TACAACAATATTCATTGGTTTTTTTATCACAGTACATGGGTTGTTACATCCACCTTGTGTT 488

QY 160 TAAAGTTGACCGGCGCATTCACATTTATTTGCGGTGCATTGAATTTGTTGGCATTTCC 219

Db 487 TCAACTGTGCTGGGCATTGTTTCGTTAATAGTGTCTGTGCACTCTGAGATTACGACAT--- 432

QY 220 CTCCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATAAATCCATCAACTAAAGAAA 279

Db 431 -----CCTCCATTGCTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGAGA 377

QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGTCAGGCGTACTCGCTAGGGTGTGTTGGT 339

Db 376 TGTGACAAAGTTC---CTGATTGGGTTGATTAAAGTGAATTCAGCTAAAGTGTAGGTG 320

QY 340 GTTTGCCCCACCCGGTGCACCTGCAGGACACACCAATCCACAGTCATGACGAACTC 399

Db 319 CTTTTCATAGCCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260

QY 400 TACCGACCATCGAAGTTATCATCCAGTACAGCCCATATACCTGCCATCTAGTAGCCCC 459

Db 259 GGCCCACTGCCATCGAAGTTGCAATTTGTTGACCCCAAAATCGAGCTCGGACTGTCTGTG 200

QY 460 TAGGGCGCATCATGACCCACATTTGCGCCCGCGATCCAAACGTCGGCACCCGCTTCGGGGT 519

Db 199 GGTTCACATTAATGCTCCAGATTGGCTGAGTGGAGCGGCTGCTCCACT--GGAGA 142

QY 520 CGATGCCGCCCAACGATGTATGGACAGTTGTTGCGTACCTCGATAGTGGCAGCAATAAGT 579

Db 141 GCGCGGCGCCAGATGTGTAGTGCATTTGTTGACATGTGCAAAAGTGGCAGCATGAGT 82
 QY 580 GAAAGTCACAAA 591
 Db 81 AACAGCTACAAA 70

RESULT 11

US-08-444-803-4/c

Sequence 4, Application US/08444803

Patent No. 5654414

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,803

FILING DATE: 19-MAY-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT 1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-444-803-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Mismatches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY	46	GGTATCTTTGTTTGA	-----GGACCTTGGG	99
Db	607	GGCATCTTTTCCCTTAA	-----GGACCTTGGG	548
QY	100	TGCAACAATATTGTTG	-----GGACCTTGGG	159
Db	547	TACACAATATTGTTG	-----GGACCTTGGG	488
QY	160	TAGTTGACAGGCGATT	-----GGACCTTGGG	219
Db	487	TCAACTGTGCTGGCAT	-----GGACCTTGGG	432
QY	220	CTCCACTTGGATTAGT	-----GGACCTTGGG	279
Db	431	-----CCTCCATTGG	-----GGACCTTGGG	377
QY	280	TGTCCAGAAATCTAAG	-----GGACCTTGGG	339
Db	376	TGTCGACAAAGTC---	-----GGACCTTGGG	320
QY	340	GTTTGGCCCCCGGGTG	-----GGACCTTGGG	399
Db	319	CTTTTCCATAGCCTTG	-----GGACCTTGGG	260
QY	400	TACACGACCATCGAAG	-----GGACCTTGGG	459
Db	259	GGCCACTGCGCATCGA	-----GGACCTTGGG	200
QY	460	TAGGGCGATCAATGAC	-----GGACCTTGGG	519
Db	199	GGTTTACATTAATGCT	-----GGACCTTGGG	142
QY	520	CGATCGCGCCCAACGA	-----GGACCTTGGG	579

Db 141 GCGCGCGCCAGACTGTAGTGGTCATTTGTGACATCTCAAAAGTGGCAGCATGAGT 82

Qy 580 GAAAGTCACAAA 591

Db 81 AACAGCTACAAA 70

RESULT 12

US-08-449-043-4/c

; Sequence 4, Application US/08449043

; Patent No. 5689044

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,043

; FILING DATE: 24-MAY-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 900 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-449-043-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 7.4e-27;

Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

Qy 46 GGTATCTTTTGTGAAAAATGGAAAAAGACGTAGGACCAAT-----GGACTTGGG 99

Db 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATCATCCAGGCCCATTTG 548

Qy 100 TGCACAAATATTTGTTCTCTCCAAATGTTGACAGGATTTTACATCTCCGGGTACTT 159

Db 547 TACAAATATTTCAATTTGTTTTTATCAGTACATGGGTTGTTATCATCCACTTGTGTTT 488

Qy 160 TAAAGTTGACCGAGGCATTCACCAATTTATTTTGGCGTGCAATTTGTTGGCAATTTCC 219

Db 487 TCAACTGTCTGGGCATTTGTTTAAATAGGTGCTGTGCACTGAGATTACGACAT----- 432

Qy 220 CTCACATTTGATTTAGTTCGGGGGAAAGTCATCGGTATATTAAATCCATCACTAAGAA 279

Db 431 -----CCTCCATTTGTCGGGCTGAAATTCATGGGATGTTAAATCCATCAACAGAGAGA 377

Qy 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAAGCGCTACTCGGCTAGGGTGTGTTGGTG 339

Db 376 TGTGCAAAAGTC---CTGATTTGGTTCATTAAGTGCAAAATCAGCTAAAGTTTAGGTG 320

Qy 340 GTTTGCCCCACCCGGTGCATCGAGGACACCAACCAATCAACCATGATGACGACCTC 399

Db 319 CTTTTCATAGCTTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTTACCTC 260

Qy 400 TACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATACCTGCGCATCGTAGTCCCC 459

Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTGACCCCAATCGAGCTGGAGCTGTTCTGTG 200

Qy 460 TAGGGCGCATCAATGACCCACATTTTGGCCCCGATGAAAGTGGCGGACCCGCTTTCGGGGT 519

Db 199 GGTTCACATTAATGCTCCAAAGATTGGCCTGAGTCGAGCCGCGCTGCTCCACCT--GGAGA 142

Qy 520 CGATGCCGCCCAACGATGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGT 579

Db 141 GCGCGGCGCCAGACTGTGTAGTGCATTTGTCACATGTCACAAAGTGGCAGCATGAGT 82
QY 580 GAAAGTCACAAA 591
Db 81 AACAGCTACAAA 70

RESULT 13
US-08-456-265A-4/c
; Sequence 4, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
; FILING DATE: 31-MAY-95
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/532,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727/DIV10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-456-265A-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 7.4e-27;
Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;
QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGTAGGACACAT-----GGACCTTGGG 99
Db 607 GGATCTTTTCCTTAAAAAATCTCGAAATAGTAGGCCACATGATCCAGGCCCATTTG 548
QY 100 TGCACAAATATTGTTGCTCTCCAAATGTGGTCAAGGATTGTACATCTCCGGGTACTT 159
Db 547 TACACAAATATTCAITGGTTTTTATCACAGTACATGGGTTGTATCATCCACCTTGTGTT 488
QY 160 TAAGTTGACAGCGGATTCACCATTTATATTTGCGGTGCAATTGAATTGTGTGCAATTC 219
Db 487 TCACTGTCTGGCAATTGTTGTTAATAGGTGCTGTGTCATCTGAGATTACGACAT- 432
QY 220 CTCACCTTGGATTAGTCGGGGGAAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAA 279
Db 431 -----CCTCCATTGGTCGGGCTGAATTCATGGGATGTTAATCCATCAACAAGAGA 377
QY 280 TGTCCCAAGAAATCTAAGTTGTTGAATGCTGCAAGCGTACTCGGCTAGGGTGTGTTGGTG 339
Db 376 TGTGCAAAAGTC---CTGATTGGGTTGATTAAAGTCAAAATTCAGCTAAAGTGTAGGTG 320
QY 340 GTTTGCCCCCACCCTGGTGCATCGAGCACACACCACCAATCACAGTCATGCACGACCTC 399
Db 319 CTTTTCATAGCTTGCACACTCTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATATCTGCCATCGTAGTGCCTC 459
Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAAAATCGAGCCTGGAGCTTCCTG 200
QY 460 TAGGGCATCAATGACCCACATTTGGCCCCGATCGAAAGTGGCGGACCCGCTTCGGGT 519
Db 199 GGTTCATTAATGCTCCAAGATTGCGCTGAGTCGAGCGCGCTGCTCCACCT--GGAGA 142
QY 520 CGATGCCGCCCAACGATGATGACAGTTGTGTGGTACCTCGATAGTGGCAGCATAAGT 579
Db 141 GGCCGGCGGCCAGACTGTGTAGTGCATTTGTTGACAAATGTCAAAGTGGCAGCATGACT 82
QY 580 GAAAGTCACAAA 591
Db 81 AACAGCTACAAA 70

RESULT 14
US-08-455-416-4/c
; Sequence 4, Application US/08455416
; Patent No. 5777200

GENERAL INFORMATION:
 APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/455,416
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT 1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 900 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-455-416-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 7.4e-27;
 Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;

QY 46 GGTATCTTTTGGAAAAATTTGAAAAAGACCTAGGACACAT-----GGACCTGGG 99
 DB 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
 QY 100 TCGAACAAATATTGTCTCTCAAAATGTGGTACAGGATTTGTTATCATCTCTCCGGTACTT 159
 DB 547 TACACAAATATTCTATGGTTTTTATCAGTACATGGTTGTTATCATCCACCTTTGTTT 488
 QY 160 TAAGTTGACAGGGCATTCACATTTATTTATTTGCGGTGATGAATTTGTGGGATTTCC 219
 DB 487 TCAACTGTCTGGGCATTTGTTCTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
 QY 220 CTCACATTTGATTAGTCGGGGCGAAAGTCATCGGTATATATAATCCATCACTAAAGAAA 279
 DB 431 -----CTCTCATTTGTCGGGTGATTTCCATGGGGATTTAAATCCATCAACAGAGA 377
 QY 280 TGTCACAGAAATCTAAGTTGTGTGAATCTGGTCCAGGGGTACTCGGCTAGGGTGTGGTG 339
 DB 376 TGTCGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAAATTCAGCTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCACCCGGTGCACCTGCAGGACACCAACCATCACCAGTCAATGCAGAACCTC 399
 DB 319 CTTTTCATAGCTTGCACACTCTACATCCCGTTACAGTCTCCAGTCTCACATATACCTC 260
 QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCTC 459
 DB 259 GGCCTATGCCATCGAAGTTGCAATTTGGTTCGACCCCAATCGAGCCCTGGACTGTCTCTG 200
 QY 460 TAGGCGCATCAATGACCCACATTTGGCCCCCATCGAAGCTCGGACCCCGTTCGGGGT 519
 DB 199 GGTTCACATTAATGCTCCAAAGATTGGCCTGAGTGGCCGCTGCTCCACT--GGAGA 142
 QY 520 CGATCGCCGCCAAACGATGTATGGACAGTTGTTGGTACCTCGCATAGTGGCAGCATAGT 579
 DB 141 GCGCGGCGCCGACGATGTGTAGTGCATTTGTTGACATGTCAAAGTGGCAGCATGAT 82
 QY 580 GAAAGTCAAAA 591
 DB 81 AACAGCTACAAA 70

RESULT 15
 US-08-455-244-4/c
 ; Sequence 4, Application US/08455244
 ; Patent No. 5789214

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr. Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary E.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-244-4

Query Match 9.7%; Score 155.2; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 7.4e-27;
Matches 334; Conservative 0; Mismatches 198; Indels 20; Gaps 4;
QY 46 GGTATCTTTGTTGAAAAAATGGAAAGACGTAGGACCAAT-----GGACCTGGG 99
Db 607 GGCATCTTTCTTAAAAAATCTGACAAATCAGTAGGCCCAATGATCCAGGCCCAATTTG 548
QY 100 TGCAACAATATTGTTGCTCTCCAAATGTTGTTACAAAGGATTTACATCTCCGGGTACTT 159
Db 547 TACACAATATTCTGTTGTTTATCACAGTACATGGGTTTGTATCCACCTTGTTT 488
QY 160 TAAATTGACCGGCAATTCACCAATTTATATTTGCCGTGCAATTTGAATTTGTGGCAATTC 219
Db 487 TCAACTGTCTGGGCATTTGCTGTTAATAGGTGCTGTCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCACTAAGAAA 279
Db 431 -----CCTCCATTGTCGGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAGCGCTACTCGCTAGGGGTGTTTGGTG 339
Db 376 TGTGACAAAGTC---CTGATTGGGTGATTAAAGTGCAATTCAGCTAAGTGTAGGTG 320
QY 340 GTTTGCCCCACCCGGTGCACTGCAGGACACCAACCAATCACAGTCTATGACGACCTC 399
Db 319 CTTTTCATAGCCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCACAATTTACCTC 260
QY 400 TACCAGCACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTCCCTC 459
Db 259 GGCCTACTGCATCGAAGTTGCAATTTGGTTTCGACCCCAATTCGAGCCTGGAGCTGTTCTG 200
QY 460 TAGGCGCATCAATGACCCCAATTTGGCCCCGATCGAAACGTCGGCACCCGCTTTCCGGGT 519
Db 199 GGTTCACATTAATGCTGCCAAGATTGGCTGAGTCGAGCGCTGCTCCACCT--GGAGA 142
QY 520 CGATCCGCCCAACGATGTATGGACAGTTGTTGGTACCTCGATAGTGGCGACGATAAGT 579
Db 141 GGCCTCGGCCAGACTGTAGGTGCATTTGTTGCAATGTCAAAAGTGGCAGCATGAT 82
QY 580 GAAAGTCACAA 591
Db 81 AACAGTACAA 70

Search completed: August 18, 2004, 16:17:34
Job time : 126.848 secs

OM nucleic - nucleic search, using sw model
Run on: August 18, 2004, 05:06:40 ; Search time 3750.05 Seconds
(without alignments)
12701.209 Million cell updates/sec

Title: US-10-051-307-1
Perfect score: 1595
Sequence: 1 gtaataagactcaactatagg.....tggtgaagtgggtgctttc 1595

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
EST:			
1:	em	estba:	
2:	em	esthum:	
3:	em	estini:	
4:	em	estmu:	
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7:	em	estro:	
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9:	gb	estl:	
10:	gb	estc:	
11:	gb	atc:	
12:	gb	est3:	
13:	gb	est4:	
14:	gb	est5:	
15:	em	estfun:	
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17:	em	gss_hum:	
18:	em	gss_inv:	
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20:	em	gss_vrt:	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 3	485	30.4	988	14	CK246326
C 4	483.2	30.3	888	14	CK278032

CK271811	EST717869	853	14	CK271811
CK252271	EST735908	899	14	CK252271
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AW039873	EST282346	649	9	AW039873
BI432833	EST535594	583	12	BI432833
BF053678	EST438908	622	10	BF053678
BG130650	EST463582	639	12	BG130650
BI922472	EST542376	667	12	BI922472
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BI921735	EST541638	669	12	BI921735
BM410787	EST585114	782	12	BM410787
CK271145	EST717223	944	14	CK271145
CK277819	EST723897	936	14	CK277819
CK279273	EST725351	916	14	CK279273
AW223507	EST300318	657	10	AW223507
BI921330	EST536716	776	12	BI921330
BI434454	EST537215	638	12	BI434454
BI434095	EST536856	757	12	BI434095
BI421330	EST531996	575	12	BI421330
AW441774	EST311170	574	10	AW441774
BI433955	EST536716	639	12	BI433955
BM403979	EST578306	660	12	BM403979
BI423179	EST533845	604	12	BI423179
BI921311	EST541214	637	12	BI921311
BI422260	EST532926	719	12	BI422260
BI921826	EST541729	720	12	BI921826
BI421946	EST532612	807	12	BI421946
AW223623	EST300434	574	10	AW223623
AW033829	EST277400	626	9	AW033829
BE432710	EST399239	629	10	BE432710
AW223970	EST300781	682	10	AW223970
AW035171	EST280433	710	9	AW035171
AW032317	EST275771	573	9	AW032317

ALIGNMENTS

RESULT 1
CK252883/c
LOCUS
DEFINITION
EST736520 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone F0CC086 5' end, mRNA sequence.
ACCESSION
CK252883
VERSION
CK252883.1 GI:39807285
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 899)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTC ACA CTA TAG.
FEATURES
source
1. .899
/organism="Solanum tuberosum"
/mol_type="mRNA"


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Db      10 TATATTTT 2

RESULT 3
CK246326/c
LOCUS
DEFINITION
EST729963 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCAL08 5' end, mRNA sequence.
ACCESSION
CK246326
VERSION
CK246326.1 GI:39793747
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 988)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from potato callus tissue
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST729964
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
1..988
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCAL08"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 30.4%; Score 485; DB 14; Length 988;
Best Local Similarity 89.0%; Pred. No. 1.5e-90;
Matches 535; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAAATGGAAAGACGTAGGACCACTGGACCTTGGGTGCAAC 105
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 GGCATCTTTGTTGAAAAATCTAGACAAATCAGTAGGACCACTGGACCTTGGGTGCAAC 542
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 AATATTGTTGTCCTCCAAATGGTGACAAAGATTGTTACATCCTCCGGTACTTTAAGTT 165
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AATATTGTTGTCCTCCGAACTGGTGACAAAGATTGTTACATCCTCCAGGTACCTAAGTG 482
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 GACACGGCATTCACCATTTATTTGCGGTGCAATTGAATTTGTTGGCATTTCCCTCCAC 225
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 AACACGACATTCACCATTTATTTAGCGGTGCAATGAATTTGCGTGGCATTTCCCTCCAC 422
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 TTGGATTAGTCGGGCGAAAGTCATCGGTATATTAATCCATCACTAAGAAATGCCCC 285
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 TAGGATTGTTGGGCGAAAGTCATCGGTATATTAATCCATCACTAAGAAATGCCCC 362
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
286 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGCGTACTCGGTAGGCTTTGGTGGTTGTC 345
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGCGTACTCGGTAGGCTTTGGTGGTTGTC 302
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
346 CCCACCGGTGCACTGACGACACACCAATCACCAGTATCGACGACCTTACAG 405
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CCCACCGGTGCACTGACGACACACCAATCACCAGTATCGACGACCTTACAG 242
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
406 CACATCAAGTTATCATCCAGTACGACCCCATACCTGCTAGTGCCTTAGCG 465
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      241 CACCATCAAGTTGCAATTAGTAGCAGCCCATATAGTGCCTATTAGTGCCCTCGGG 182
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
466 CATCAATGACCCACATTTGGCCCCCGATCGAAACGTCGG-CACCCGCTTTGGGGTGCATG 524
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 CATTGATAACCCATGTCGTGCTCGATCGAGACGTCGGCCACCGCTATCGGGTGCATG 122
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
525 CGCCCAACAGATGATGACAGAGTTGTTGGGTACCTCGATAGTGGCAGCATAGTGAAG 584
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 CGCCCAACAGATGATGACAGAGTTGTTGGGTACCTCGATAGTGGCAGCATAGTGAAG 62
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
585 TCACAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCATGTTTGTGAAA 644
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 TCACAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
645 T 645
Db      1 T 1

RESULT 4
CK278032/c
LOCUS
DEFINITION
EST724110 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAE351 5' end, mRNA sequence.
ACCESSION
CK278032
VERSION
CK278032.1 GI:39835010
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 888)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE
Generation of ESTs from abiotic stressed potato tissue
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST724111
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
1..888
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAE351"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,

```

12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 30.3%; Score 483.2; DB 14; Length 888;
Best Local Similarity 89.3%; Pred. No. 3.5e-90;
Matches 532; Conservative 0; Mismatches 63; Indels 1; Gaps 1;
QY 46 GGTATCTTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTGCAAC 105
DB 597 GGCATCTTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTGCAAC 538
QY 106 AATATTGTTGTCCTCAAAATGTTGTAAGGATGTTTACATCTCTCCGGGTACTTTAAGTT 165
DB 537 AATATTGTTGTCCTCAAAATGTTGTAAGGATGTTTACATCTCTCCGGGTACTTTAAGTT 478
QY 166 GACGAGGCAATTCACCATTTATATTTCCCTGCAATGCAATGTTGTCATTTCCCTCCAC 225
DB 477 AACGAGGCAATTCACCATTTATATGCGGTGCAATGCAATGTTGTCATTTCCCTCCAC 418
QY 226 TTGATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCAATCAAGAAATGTCCTCC 285
DB 417 TAGGATTGTTGGGCGAAAGTCAATCGGTATATTAATCCATCAATCAAGAAATGTCCTCC 358
QY 286 AGAATCTAAGTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTG 345
DB 357 AGAATCTAAGTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTG 298
QY 346 CCCACCGGTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 405
DB 297 CCCACCGGTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 238
QY 406 CACCATCGAAGTTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 465
DB 237 CACCATCGAAGTTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 178
QY 466 CATCAATGACCCCATTTGGCCCGGATCGAAACCTCGG - CACCCGCTTTGGGGTTCGATG 524
DB 177 CATGATTAACCATGTTCTGGCTCGATCGAGACGTCGCGCACCCGCTATCGGGTTCGATG 118
QY 525 CGGCCCAACCATGATGAGACAGTTGTTGCTACCTCGATATGTCGACGACATAAGTGAAG 584

RESULT 5
CK271811/c
LOCUS
DEFINITION
EST171889 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAD143 5' end, mRNA sequence.
CK271811
ACCESSION
VERSION
KEYWORDS
SOURCE
Solanum tuberosum (potato)
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 853)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST171890
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org

FEATURES
Source

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..853
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAD143"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
5hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 5hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Query Match 30.3%; Score 482.6; DB 14; Length 853;
Best Local Similarity 89.1%; Pred. No. 4.8e-90;
Matches 532; Conservative 0; Mismatches 64; Indels 1; Gaps 1;
QY 46 GGTATCTTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTGCAAC 105
DB 597 GGCATCTTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTGCAAC 538
QY 106 AATATTGTTGTCCTCAAAATGTTGTAAGGATGTTTACATCTCTCCGGGTACTTTAAGTT 165
DB 537 AATATTGTTGTCCTCAAAATGTTGTAAGGATGTTTACATCTCTCCGGGTACTTTAAGTT 478
QY 166 GACGAGGCAATTCACCATTTATATTTCCCTGCAATGCAATGTTGTCATTTCCCTCCAC 225
DB 477 AACGAGGCAATTCACCATTTATATGCGGTGCAATGCAATGTTGTCATTTCCCTCCAC 418
QY 226 TTGATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCAATCAAGAAATGTCCTCC 285
DB 417 TAGGATTGTTGGGCGAAAGTCAATCGGTATATTAATCCATCAATCAAGAAATGTCCTCC 358
QY 286 AGAATCTAAGTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTG 345
DB 357 AGAATCTAAGTTGTTGAAAGAAATGGAAGAACGAGGAGGACACACATGGAACCTTGGGTG 298
QY 346 CCCACCGGTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 405
DB 297 CCCACCGGTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 238
QY 406 CACCATCGAAGTTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 465
DB 237 CACCATCGAAGTTACATCTGCAAGAACCCACCAATCAATCAAGGATGTTGCAATGCAATGCAATG 178
QY 466 CATCAATGACCCCATTTGGCCCGGATCGAAACCTCGG - CACCCGCTTTGGGGTTCGATG 524
DB 177 CATGATTAACCATGTTCTGGCTCGATCGAGACGTCGCGCACCCGCTATCGGGTTCGATG 118
QY 525 CGGCCCAACCATGATGAGACAGTTGTTGCTACCTCGATATGTCGACGACATAAGTGAAG 584

[illegible]

Query Match	30.0%;	Score 478.8;	DB 12;	Length 739;
Best Local Similarity	89.3%;	Mismat. No. 3e-89;		
Matches 527;	Conservative	0;	PredMatches 62;	Indels 1; Gaps 1;

QY	46	GGTATCTTTGTTTGAATAAATTGGAAAAGACGTAGGACCACATCGACTGGCTGGTGCAAC	105
Db	590	GGCATCTTTGTTTGAATAAATCTGCACAATCAGTAGGACCACATCGACTGGCTGGTGCAAC	531
QY	106	AATATTGTTGTCCTCCAAATGTGGPACAGAATTGTTACATCTCTCCGGGTACTTTTAAGTT	165
Db	530	AATATTGTTGTCCTCCGAACGTGGTACAAAGGATTGTTACATCTCTCCAGTACCCCTAAGTG	471
QY	166	GACCAGGGCATTCACCATTTATATTGCGCGGCAATGGAATTGCTGGCATTTCCCTCCAC	225
Db	470	AACCAGGACATTCACCATTTATATTGCGCGGCAATGGAATTGCGTACATTTCCCTCCAC	411
QY	226	TTGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATFCCATCAACTAAAGAAATGTCCC	285
Db	410	TAGGANTGGTTGGGCGAAAGTCATCGGAATATTAAATFCCATCGACTAAAGAAATGTCCC	351
QY	286	AGAAATCTAGTTGTTGNACTGGTCCAAGGGCTACTCGGTAGGGTGTGTTGGTGGTTTGC	345
Db	350	AGAAATCTAGTTGTTGCTGAACGTGGTCCAAGGGCTACTCGGTAGGGTGTGTTGGTGGTTTGC	291
QY	346	CCCCACCGGTGCATCGCAGGACACACCAACAATCACCAAGTCATGCCAGAACCTCTACCA	405
Db	290	CCCCACCGGTACATTCGAAGACCCCAACAATCACCAAGTTGGCATGAACCTCTGCCAG	231
QY	406	CACCATCGAAGTTACATCCAGTACGACCCCATAPACTGTGCATCGTAGTGCCCTTAGCGG	465
Db	230	CACCATCAAAAGTTACAAATTAGTAGACGCCCATATACGTGTCATTTTAGTACCCCTCGGG	171
QY	466	CATCAATGACCCCATTTGGCCCCGATCGCAAAAGCTCG - GCACCGCTTTTCGGGGTCGATG	524
Db	170	CATTGATGACCCATGTCGCGCTCGATCGAGAGCTGCACCCGCCCTATCGGGGTGCGATG	111
QY	525	CCGCCCAAACGATGATGACAGTTGTTGGCTACCTCGATAGTGGCAGCATAAAGTGAAAG	584
Db	110	CCGCCCACACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAAAGTGTAAG	51
QY	585	TCACAAAGCAAGNAGGAGAAACAAAGAAAGTCTCAAGTAGGCCCATG	634
Db	50	TCACAAAGCAAGNAGGAGAAACAAAGAAAGTCTCAAGTAGGCCCATG	1

RESULT 8	AW039873/c
LOCUS	AW039873
DEFINITION	EST28246 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA clone cUE1J13, mRNA sequence.
ACCESSION	AW039873
VERSION	AW039873.1
KEYWORDS	GI:5898627
SOURCE	EST.
ORGANISM	Lycopersicon esculentum (tomato)
REFERENCE	Lycopersicon esculentum
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 649)
TITLE	D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J., Ronning C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Praser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
JOURNAL	Generation of ESTs from tomato leaf tissue
COMMENT	Unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence. Location/Qualifiers 1 . 649

FEATURES	source
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 583)
Restrepo,S., Griffiths,H.M., Smart,C.D., Chiemingo,A.,
Bougrit,O., Buell,C.R., Ronning,C.M., Fry,W.E., and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: M13F-R.

FEATURES

source	Location/Qualifiers
	1..583
	/organism="Solanum tuberosum"
	/mol_type="mRNA"
	/cultivar="Kennebec"
	/db_xref="taxon:4113"
	/clone="PPCM35"
	/tissue_type="leaf"
	/dev_stage="6 week old"
	/lab_host="SOLR"
	/clone_lib="P. infestans-challenged potato leaf, compatible reaction"
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN	Query Match	29.4%	Score 468.8	DB 12	Length 583
	Best Local Similarity	89.1%	Pred. No. 3.8e-87		
	Matches 517	Conservative 0	Mismatches 62	Indels 1	Gaps 1
Qy	67	TGGRAAGACGTAGGACCATCGACCTTGGTGCAACATATTTGTTGCTCTCAATG	126		
Db	581	TCGCAAAATCAGTAGGACCATCGACCTTGGTGCAACATATTTGTTGCTCTCAATG	522		
Qy	127	TGGTACAAAGGATTTGTTACATCTCTCGGGTACTTTTAAGTTGACCAAGGCATTCACCATTTA	186		
Db	521	TGGTACAAAGGATTTGTTACATCTCTCGAGTACCTTAAGTGAACACAGGCATTCACCATTTA	462		
Qy	187	TATTTGGGTGCATGTGAATTTGTGTGGCATTTCCCTCCACTTGGGATTTAGTCGGGGCGAAG	246		
Db	461	TATTAGCGGTGCAATGAATTCGGTGCACATTTCCCTCCACTAGGATTTGGTTGGGGCGAAG	402		
Qy	247	TCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCCAGAAATCTAAAGTTGTGAACT	306		
Db	401	TCATCGGAAATTATTAATCCATCGACTTAAGAAATGTCCCAGAAATCTAGGTTGCTGAACT	342		
Qy	307	GGTCCAAAGCGGTACTCGGCTAGGGTGTGTTGGTGGTTTGGCCCAACCGGTGCACGTGCAAG	366		
Db	341	GGTCCAAAGCGGTACTCGGCTAGGGTGTGTTGGTGGTTTGGCCCAACCGGTGCACATTCGAAG	282		
Qy	367	CACCAACCAATCACCAGTCATGCACGAACCTCTACACAGCACCATCGAAGTTACATCCAG	426		
Db	281	CCCAACCAATCACCAGTTTGGGCATGAACCTCTGCCAGCACCATCAAAAGTTACAATTAG	222		
Qy	427	TACGACCCCATATACCTGCCATCGTGTGTCGCCCTTAGGCGCATCAATGACCCACATTTGGC	486		
Db	221	TACGACCCCATATACCTGCCATTTAGTACCCCTCGGCGCATGTATGACCCCATGCTGCG	162		

[illegible]

Qy	226	TTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAGAAGAAATGTCCC	285
Db	422	TAGGATTTGGTCGGGGCAAAAGTCATTTGGTATATTAATCCGTCAACTAAGAAGAAATGTCCC	363
Qy	286	AGAAATCTAAGTTGTTGAACCTGGTCCAAGCGTACTCGGCTAGGGTGTTTGGTGGTTTGC	345
Db	362	AGAAATCTAGGTTGTTTAAACTGATTTCAAGGCGATATTCGGCCAGGGTGTTTGGCGGTTTAC	303
Qy	346	CCCAACCCGGTCACCTGCGAGGACACACCAAACTACCAAGTCATGACAGCAACTCTTACAG	405
Db	302	CCCAACCCGGTACACTGCAAGACTCCACCAACTACACGCTGTACAGAAGCAACTCTTACCAG	243
Qy	406	CACCATCGAAAGTTACATCCAGTACGAGCCCAATATACCTGCCATCGTAGTGCCTCCCTAGCG	465
Db	242	CACCATCAAGTTTGCATTTAGTACGACCCCATATACGTGCCATCTTAGTGCCCTCGGTG	183
Qy	466	CATCAATGACCCACATTTGGCCCCGATCGAAAAGTCGG-CACCCGGTTTTCGGGGTCGATG	524
Db	182	CATTGATGACCCCAAGTTTGACCTCGATCGAGAGCGTCGGCCACCGCTATTCGGGGTTGATG	123
Qy	525	CGGCCCAACAGATGTATGGACAGTTGTTGGCGTACCTCGATAGTGGCAGCATAAGTGAAG	584
Db	122	CGGCCACAGCGTGATGGACAGTTGTTTCCGACCTCAAAAGAGGTAGCATTAAGTATAAAG	63
Qy	585	TCACAAAAGCAAGGGAGAAAACAAAAGAGATCTCAAGTAGGCCCATGTTTT	637
Db	62	TCACAAAAGCAAGGAGGAGAAAACAAAAGAAATCTCAATAGGCCCATGTTT	10

AUTHORS	van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C., Roning,C. and Tanksley,S.
TITLE	Generation of ESTs from tomato crown gall tissue
COMMENT	Unpublished (2001)
FEATURES	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html . Location/Qualifiers 1. . 639 /organism="Lycopersicon esculentum" /mol_type="mRNA" /cultivar="TA496" /db_xref="taxon:4081" /clone="cfoetA9" /tissue_type="crown gall" /dev_stage="crown galls from full-grown plants (8 wks old)" /lab_host="SOLR"
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REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
RESULT 12	
B1922472/c	
LOCUS	
DEFINITION	

ORIGIN

FEATURES

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1..667
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/clone="cLEC77J15"
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/clone_lib="tomato callus"
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XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN
Query Match      29.0%; Score 463.2; DB 12; Length 667;
Best Local Similarity 86.8%; Pred. No. 5.4e-86;
Matches 521; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 47  GTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGAGACCTTTGGGTGCAACA 106
Db    |||
QY 107 ATATTGTTGCTCCCAATGTGTACAGGATTTGTACATCCTCCGGGTACTTTAAGTTG 166
Db    |||
QY 541 ATATTGTTGCTCCGAACTGGTACAGGATTTGTACATCCTCCGGGTACCTTAAGTGA 482
QY 167 ACCAGGCAATTCACCATTTATTTGCGGTGCATTTGAATTTGTGGGCATTTCCCTCCACT 226
Db    |||
QY 481 ACCAGGCAATTCACCATTTATTTAGCGTACATGAATTTGCATGGCATTTCCCTCCACT 422
QY 227 TGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATTCATCACTAAAGAAATGCCCCA 286
Db    |||
QY 421 AGGATTGGTCGGGGCGAAAGTCATTGGAATATTAAATCCATCGACTAAAGAAATGCCCCA 362
QY 287 GAAATCTAAGTTGTTGAACTTGTCCTCAAGGCGTACTCGGGTAGGGTGTTCGTGGTTGGC 346
Db    |||
QY 361 GAAATCTAAGTTGCTAAACTGGTCCAGGGGTACTCGGCCAGGGTGTTCGTGGTTGGC 302
QY 347 CCACCCGGTGCACCTGCAGGACACACCAATACACAGTATGTCAGCAAACTCTTACCAGC 406
Db    |||
QY 301 CCACCCGGTACATTGCAAGACCCACCAATCACACAGTCTGCATGAACCTCTTACCAGC 242
QY 407 ACCATCGAAGTTACATCCAGTACGACCCCATATACCTGCCATCGTAGTGCCTTAGCGGC 466
Db    |||
QY 241 ACCATCGAAGTTGCAATTCGTACACCCCATATACGTGCCATCTTAGTGCCTTCGGTGC 182
QY 467 ATCAATGACCCACATTTGGGCCCCGATCGAAACGTCG-GCACCCCGCTTTCCGGGGTCGATGC 525
Db    |||
QY 181 ATTGATGACCCATGTTTGGCTCGATCAAGCGTTCGACCCCGCTATTGGGGTTCGACGC 122
QY 526 CGGCCAAACGATGTATGGAAGTTGTTGGTACTCTCGATAGTGGCAGCATTAAGTGAAGT 585
Db    |||
QY 121 CGGCCACAGCGTGTATGGAAGTTGTTGCGTACTTCGAAAGTGGCAGCATTAAGTGAAGT 62
QY 586 CACAAAAGCAAGGAGGAGAGAAACAAAGAAGATCTCAAGTAGGCCCATGTTTGTGGAAT 645
Db    |||
QY 61  CACAAAAGCAAGGAGGAGAGAAACAAAGAAGATCTCAAGTAGGCCCATGTTTGTGGAAGT 2

RESULT 13
AW031249/c
LOCUS
DEFINITION
EST274624 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLEC34F24 similar to osmotin-like protein TPM-1 precursor (PR P23),
mRNA sequence.
ACCESSION
VERSION
AW031249
KEYWORDS
EST.

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QY 546 AGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCAAGTCAAAAGCAGAGGGGAGA 605
Db |||||
QY 103 AGTTGTTGGTACCTCGAAGAGTGGCAGCATAGTGAAGTCAAAAGCAGAGGGGAGA 44
Db |||||
QY 606 AAACAAAAGAGATCTCAAGTAGGCCATGTTTGTGTAATTT 647
Db |||||
QY 43 AAACAAAAGAGATCTCAAGTAGGCCATGTTTGTGGAATAT 2
Db |||||

RESULT 14
CAS14039/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE
AUTHORS
Lee, S.-Y., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
TITLE
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL
Unpublished (2001)
COMMENT
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
Plate: 015 row: D column: 01.

FEATURES
source
1..598
/organism="Capsicum annuum"
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ORIGIN
Query Match 28.7%; Score 457.2; DB 14; Length 598;
Best Local Similarity 86.7%; Pred. No. 9.8e-85;
Matches 515; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 46 GGTATCTTTGTTGAAAATTTGAAAAGACGTAGGACACATGGACCTTGGGTGCAAC 105
Db |||||
QY 594 GGCATCTTTCTTGAATAATTTGACAACTCAGTAGGACACATGGACCTTGGGTGCAAC 535
Db |||||
QY 106 AATATTGTTGTCCTCAAAATGTGTACAGGATTTTACATCTCTCCGGGTACTTTAAGTT 165
Db |||||
QY 534 AATATTGTTGTCCTCAAAATGTGTACAGGATTTTACATCTCTCTGGTACCTGAGTG 475
Db |||||
QY 166 GACCAGGGCATTCACATTTATATTTCCTCGTCAATTTGAATGTGTCATTTCCCTCCAC 225
Db |||||
QY 474 AACAGGGCATTCACATTTATATTTCCTCGTCAATTTGAATGTGTCATTTCCCAACAC 415
Db |||||
QY 226 TTGATTAGTTCGGGGGAAAAGTCATCGGTATATTAATCCATCAATTAAGAAATGTCCC 285
Db |||||
QY 414 TAGGATTGTTGTCGGTGGCAAGTCAATCGTATGTGAATCATGACATTAAGAAATGTCCC 355
Db |||||
QY 286 AGAAATCTAGTTGTTGAATCTGAGCGGTACTCGGCTAGGGTGTGTTGGTGTTCG 345
Db |||||
QY 354 AGAAATCTAGTTGTTGAATCTGAGCGGTACTCGGCTAGGGTGTGTTGGTGTTCG 295
Db |||||
QY 346 CCCACCGGTGCACTGCGAGGACACACCAATCACCAGTCATGCAAGACCTCTACCAAG 405
Db |||||
QY 294 CCCACCGGTGCACTGCGAGGACACACCAATCACCAGTCATGCAAGACCTCTACCAAG 235
Db |||||
QY 406 CACCATCGAAGTTACATCCAGTAGGACCCCATATACCTGCCATCGTAGTGCCCTAGGCG 465
Db |||||

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Db 234 AACCATCGAAGTTGCAATTAGTACACCCCATATAGTGGCCATCTGCTCCTGGTGGG 175
QY 466 CATCAATGACCCACATTTGGCCCCGATCGAAACGTGCGCACCCGCTTTC-GGGGTCGATG 524
Db |||||
QY 174 CATTGATGTCAGGTCTGGCCTCGATCAAGAGCTGACCGCCACCTACGGGGTTCGATG 115
Db |||||
QY 525 CGCCCCAAACGATGTATGACAGTTGTTGCGTACCTCGATAGTGGCAGCATAGTGAAG 584
Db |||||
QY 114 CGCCCCAAACGATGTATGACAGTTGTTGCGACCTCGAAAGTGGCAGCATAGTGAAG 55
Db |||||
QY 585 TCACAAAAGCAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTG 638
Db |||||
QY 54 TCACAAAAGCAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTG 1

RESULT 15
AW032915/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Lycopersicon.
REFERENCE
AUTHORS
Alcala, J., Vrebalov, J., White, R., Matern, A. L., Vision, T.,
Holt, I. E., Liang, F., Upton, J., Craven, M. B., Bowman, C. L., Ahn, S.,
Ronning, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D. and
Giovannoni, J.
TITLE
Generation of ESTs from tomato callus tissue
JOURNAL
Unpublished (1999)
COMMENT
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
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/clone_lib="tomato callus, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLec - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN
Query Match 28.5%; Score 454.4; DB 9; Length 583;
Best Local Similarity 87.6%; Pred. No. 3.8e-84;
Matches 508; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 67 TGGAAAAGACGTAGGACCAACATGGTGGTGCACCAATATTGTTGCTCTCAATG 126
Db |||||
QY 581 TCGCAAAATCAGTAGGGCCACATGGACCTTGTGTGCAACAAATATTGTTGCTCTCGAAG 522
Db |||||
QY 127 TGGTACAGGATTTGATACATCTCCGGGTACTTTAAGTTGACCGGGCATTCACCAATTA 186
Db |||||
QY 521 TGGTACAGGATTTGATACATCTCCGGGTACTTTAAGTTGACCGGGCATTCACCAATTA 462
Db |||||

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QY	187	TATTTGCCGTGCAATTGAATTTGTGTGGCAATTCCTCCCACTTGATGTGCGGGCGAAAG	246
DB	461	TATTAGCCGTCAAAATGAATTTGATGGCAATTCCTTCCACTAGGATTTGGTTCGGGGCCAAAG	402
QY	247	TCATCGGTATATTAAATCCATCAACTAAAGAAATGCCAGAAATCTTAAGTTTGTGAACCT	306
DB	401	TCATTGGGAATATTAAATCCATCGACTAAAGAAATGTCCAGAAATCTAGTTTGTATAACT	342
QY	307	GGTCCAAGCGCTACTCGGCTAGGGTGTTTGGTGGTTTGGCCCAACCGGTGCACTGCAGA	366
DB	341	GGTCCAAGCGCTACTCGGCGAGGGTGTTTGGTGGTTTGGCCCCACCGGTACATTGCAAGA	282
QY	367	CACCAACCAATCACCAGTCATGCGACGACCTCTACCAAGACCATCGAAGTTTACATCCAG	426
DB	281	CCCCACCAATCACCAGTCTGACATGAACCTCTACCAAGACCATCAAAAGTTGCAATTGG	222
QY	427	TACGACCCCATATACGTGCGCATCTAGTGCCTCTAGCGCGCATCAATGACCCCATTTGGC	486
DB	221	TACGACCCCATATACGTGCGCATCTAGTGCCTCTAGTGCCTCTGGTGCATTGATGCCCATGTTGGC	162
QY	487	CCCGATCGAAACGTGCG - GCAACCGGCTTTGGGGTTCGATGCGCGCCAAACGATGTATGGAC	545
DB	161	CTCGATCAAGACGTGCAACCAACCGCTATTGGGGTTCGACGCGCCCGACAGCGTGTATGGAC	102
QY	546	AGTTGTGGGTACCTCGATAGTGGCAGCATAAAGTGAAGTCAAAAAGCAAGAGGGAGA	605
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QY	606	AAACAAAAGAGATCTCAAGTAGCCCAATGTTTGTGAAAT	645
DB	41	AAACAAACAGAGATCTCAAGTAGGCCATGTTTGTGAACT	2

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Job time : 3756.05 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 6053.11 Seconds
(without alignments)
11442.406 Million cell updates/sec

Title: US-10-051-307-2
Perfect score: 1598
Sequence: 1 gtaatagactcactatagg.....tggtgaagtgggtgctttc 1598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb_ba.*
- 2: gb_htg.*
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- 7: gb_ph.*
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- 9: gb_pr.*
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- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
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- 32: em_htg_other.*
- 33: em_htg_mus.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1598	100.0	1598	6	AX665979 Sequence
2	1482.2	92.8	1595	6	AX665978 Sequence
3	1334.4	83.5	1546	6	AX665980 Sequence
C 4	689.6	43.2	2659	8	SC81OLP
C 5	531.4	33.3	2638	8	SC13OLP
C 6	525.8	32.9	1304	8	AF033743
C 7	477.4	29.9	901	8	SC05MLP
C 8	469.2	29.4	2033	8	NTOSPR
C 9	468.8	29.3	1549	6	NTAP24G
C 10	468.8	29.3	3033	6	AR037158
C 11	468.8	29.3	3033	8	S40046
C 12	449.8	28.1	729	8	AF473702
C 13	449.6	28.1	917	8	AY035955
C 14	449.4	28.1	744	8	AF450276
C 15	448.4	28.1	818	8	AY007309
C 16	446.6	27.9	977	8	SCA81OLP
C 17	440.2	27.5	937	8	AF297646
C 18	438	27.4	856	8	CAN297410
C 19	425.6	26.6	832	8	LEPM1M
C 20	419.8	26.3	883	6	AL6780
C 21	419.8	26.3	883	6	AR027097
C 22	419.8	26.3	883	6	AR103205
C 23	419.8	26.3	884	6	AL6782
C 24	419.8	26.3	884	6	AR027098
C 25	419.8	26.3	884	6	AR103206
C 26	419.8	26.3	961	8	NTAP24
C 27	419	26.2	845	8	LEPRPA
C 28	417.8	26.1	741	6	A83550
C 29	417.8	26.1	741	6	BD082734
C 30	414	25.9	928	8	S44889
C 31	412.6	25.8	917	8	TOMNP24
C 32	398.8	25.0	971	8	AF376058
C 33	391.8	24.5	738	8	NTOSMOTIN
C 34	388.6	24.3	541	8	AY256440
C 35	388.4	24.3	542	8	AY256441
C 36	387.8	24.3	593	8	AY256429
C 37	387.4	24.2	567	8	AY256439
C 38	386.6	24.2	526	8	AY256436
C 39	386.2	24.2	538	8	AY256431
C 40	383.8	24.0	535	8	AY256434
C 41	382	23.9	510	8	AY256425
C 42	382	23.9	539	8	AY256430
C 43	380.8	23.8	621	8	AF450277
C 44	378.4	23.7	561	8	AF548357
C 45	375.4	23.5	3127	8	TOBNP50

ALIGNMENTS

RESULT 1
AX665979
LOCUS AX665979 1598 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2 from Patent WO02059333.
ACCESSION AX665979
VERSION AX665979.1 GI:29290848
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM
Zukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Dai,Z., Shi,L. and Hooker,B.S.
TITLE Gene promoters isolated from potato and use thereof

JOURNAL Patent: WO 02059333-A 2 01-AUG-2002;
Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

FEATURES
source
Location/Qualifiers
1. .1598
/organism="Solanum tuberosum"
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ORIGIN

Query Match 100.0%; Score 1598; DB 6; Length 1598;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAATACGACTCACTATAGGCGACGCGTGGTGCAGCGCCCGGGCTGGTATCTTTGTTGA 60
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QY 121 CAATATGCTGACAGGATGTTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTCAC 180
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QY 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCGCCAAGATCTAAGTTGT 300
DB 241 CGAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCGCCAAGATCTAAGTTGT 300

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QY 361 GCAGACACCAACCAATCACTAGCTGATGACGAACTCTACGACGACCAACGAGTTAC 420
DB 361 GCAGACACCAACCAATCACTAGCTGATGACGAACTCTACGACGACCAACGAGTTAC 420

QY 421 ATCCAGTACGACCCCAATATACGTCGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
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QY 781 TTGGTAAACGTTGAGGTGGAATAATGTAAGACCGGCTTAATTAATTTATTTATGA 840
DB 781 TTGGTAAACGTTGAGGTGGAATAATGTAAGACCGGCTTAATTAATTTATTTATGA 840

QY 841 ATATAGCCTATAGTTACAGTTACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 900
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QY 961 TGGCCAAAGTCTTTCGATCTTATCTATGCGCAATTTTACTTTTACGTTCTAGCCTTC 1020
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QY 1021 TAGGTACACAGTTTGAACATAAATAATCAATAAATAATGAAGTAAATAATTTAGTTT 1080
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QY 1081 TTCAATATTTAGTGTAGTATCTTTTGTAGATCAATCTGAAATATACAAACCATTCGAT 1140
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QY 1141 TTTAAATACCAACCAATCTGCTAATGGGAAGTCTATGTGATTCGTGGCAAGTGTTC 1200
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QY 1201 ATTATTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1260
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QY 1261 CTATTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1320
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QY 1321 GGAGCATGGATATATTTACTAATTAATAAATAATGGGAGGAATGATCGAAGCAATCA 1380
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QY 1381 AGCTTATGTCGATCCACATAGGATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1440
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QY 1441 GATCATGTACATTCAGTTTAAATAAATAATCTCTATAAATACTGTCTATCCCTCTTAAAC 1500
DB 1441 GATCATGTACATTCAGTTTAAATAAATAATCTCTATAAATACTGTCTATCCCTCTTAAAC 1500

QY 1501 CAAATACATCTTAACACACAAATAAATACTTAGATTCCTTAAAGAAATGAGAAATTA 1560
DB 1501 CAAATACATCTTAACACACAAATAAATACTTAGATTCCTTAAAGAAATGAGAAATTA 1560

QY 1561 TGGAGGCAAAATAAGTCTATGTTGAGTTGGTGTCTTC 1598
DB 1561 TGGAGGCAAAATAAGTCTATGTTGAGTTGGTGTCTTC 1598

RESULT 2

AX665978
LOCUS AX665978 1595 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1 from Patent WO02059333.
ACCESSION AX665978
VERSION AX665978.1 GI:29290847

KEYWORDS

SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

1
Dai, Z., Shi, L. and Hooker, B.S.
Gene promoters isolated from potato and use thereof
Patent: WO 02059333-A 1 01-AUG-2002;
Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)

FEATURES

source
1. .1598
/organism="Solanum tuberosum"
/mol_type="unassigned DNA"
/db_xref="taxon:4113"

ORIGIN


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Query Match      92.8%; Score 1482.2; DB 6; Length 1595;
Best Local Similarity 96.7%; Pred. No. 2.5e-298;
Matches 1546; Conservative 0; Mismatches 48; Indels 5; Gaps 3;

QY 1 GTAATACGACTCAGTATAGGCGACCGGTGGTCGACGGCCCGGCTGGTATCTTTGTTGA 60
DB 1 GTAATACGACTCAGTATAGGCGACCGGTGGTCGACGGCCCGGCTGGTATCTTTGTTGA 60

QY 61 AAAAATTCGAAAGAACCTAGGACACATGACGCTTGGGTGCAACATATTTGTTGCTC 120
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DB 121 CAAATGTCGTACAAAGGATTTTACATCCTCCGGGTACTTTTAAGTGTGACTAGGACATTCAC 180

QY 181 CATTTATATTTGCGGTGCAATGAAATGTGGCATTTCCCTCCACTTGGATAGTCGGG 240
DB 181 CATTTATATTTGCGGTGCAATGAAATGTGGCATTTCCCTCCACTTGGATAGTCGGG 240

QY 241 CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGAAATCTAAGTTGT 300
DB 241 CGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCACAGAAATCTAAGTTGT 300

QY 301 TGAATCGTCCAAAGCGTACTCGGCTAGGCTGTTTGGTGGTTTGCACCACCGGTGCACT 360
DB 301 TGAATCGTCCAAAGCGTACTCGGCTAGGCTGTTTGGTGGTTTGCACCACCGGTGCACT 360

QY 361 CGAGACACACCAACCAATCAGTCATGACGACCTCTACAGCAGCCACCGCAAGTTAC 420
DB 361 CGAGACACACCAACCAATCAGTCATGACGACCTCTACAGCAGCCACCGCAAGTTAC 420

QY 421 ATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCGCATCAATGACCCACA 480
DB 421 ATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCGCATCAATGACCCACA 480

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DB 481 TTTGGCCCGATCGAAACGTCGGACCGCTTTTCGGGTCGATCGGCGCCCAACGATGTA 540

QY 541 TGGACAGTTGTTGGCGGTACTCGATAGTACAGCATAGTAAAGTGAACAAAGCCAGA 600
DB 541 TGGACAGTTGTTG - CGTACCTCGATAGTGCAGCATAGTAAAGTGAACAAAGCCAGA 598

QY 601 AGGAGAAACCAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTCGACA 660
DB 599 AGGAGAAACCAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTTATATGTCGACA 658

QY 661 AATTATTTTGTACTTTATATATAGGATATGCGGCTTTTGGCCTACGATATTAAT 720
DB 659 AATTATTTTGTACTTTATATATAGGATATGCGGCTTTTGGCCTACGATATTAAT 718

QY 721 CGTATTATACAAATATCATCTTTGACTAATTATAAACGAAATATATTACAATATGAT 780
DB 719 CGTATTATACAAATATCATCTTTGACTAATTATAAACGAAATATATTACAATATGAT 778

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DB 779 TTGTTAAACGTTAGGTGGAATAATGATATAGAGCGGCTTAATTAATTTATTTATGA 838

QY 841 ATATAGCCTATAGTTTACAAAGTTAACTTTATTTGTTGATACCTTTGACATATACTCTGT 900
DB 839 ATATAGCCTATAGTTTACAAAGTTAACTTTATTTGTTGATACCTTTGACATATACTCTGT 898

QY 901 AACGTGACGGAATTTTCTTAAATCTAAATATTAATAAGACGCTATTTTCACTTTTCG 960
DB 899 AACGTGACGGAATTTTCTTAAATCTAAATATTAATAAGACGCTATTTTCACTTTTCG 958

QY 961 TGGCCAAAGTCTCTGCACTATCTATGATGCCATTTTACTTTTATCGTTCAGCCCTC 1020
DB 959 TGGCCAAAGTCTCTGCACTATCTATGATGCCATTTTACTTTTATCGTTCAGCCCTC 1018

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DB 1019 TAGGTACAGTTTGAACATAAAAAATCATAAAAATTTGAAAGTAAAAATTTAGTTTTTTT 1078

QY 1081 TTCAATTAATCTCGTATGATCAATTTGTTAGATCAATCTGAAATATACAAACCAATTCGAT 1140
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QY 1141 TTTAAATACCAACCACTTCGCTTAATTTGGGAGTCTATGATTTGTTGCGCAAGT-GTTT 1199
DB 1139 TTTAAATACCAACCACTTCGCTTAATTTGGGAGTCTATGATTTGTTGCGCAAGTGGTTT 1196

QY 1200 GATTATTTCTAGTCTAGATTTGGAGTCACAACTTTTGTAGTCAAAATATCTATTTAAAGAACC 1259
DB 1197 GATTATTTCTAGTCTAGATTTGGAGTCACAACTTTTGTAGTCAAAATATCTATTTAAAGAACC 1256

QY 1260 CTTATTGATGCAAAATATCTATTTAAAGAACCCTATTTCACTTTTATTTTACGAT 1319
DB 1257 CTTATTGATGCAAAATATCTATTTAAAGAACCCTATTTCACTTTTATTTTACGAT 1316

QY 1320 CGAGCATGATATATTTACTAATTTAAATTTAAATTTGGAGGATTCATCGACAGCCATC 1379
DB 1317 CGAGCATGATATATTTACTAATTTAAATTTAAATTTGGAGGATTCATCGACAGCCATC 1376

QY 1380 AGCTTATCGTCGATCCACATTTAGGATAACGTTAGTATGGCTGTTTATAGAGAAACAAGT 1439
DB 1377 AGCTTATCGTCGATCCACATTTAGGATAACGTTAGTATGGCTGTTTATAGAGAAACAAGT 1436

QY 1440 GGATCATGTACATTTGAGTTAAATATCTCTTATAAATACCTGCTCTCTCTTAA 1499
DB 1437 GGATCATGTATATTTAGTTTAAATATCTCTTATAAATACCTGCTCTCTCTTAA 1496

QY 1500 CCAATATCATCTAACACACAAATATAAACTTTAGATTTCTTTAAAGAAATTCGAGAAATTA 1559
DB 1497 CTAATGTCATCTAACACACAAATATAAACTTTAGATTTCTTTAAAGAAATTCGAGAAATTA 1556

QY 1560 ATGAGGCAATTAAGTCTATGTTGAGGTTGGTCTTTC 1598
DB 1557 ATGAGGCAATTAAGTCTATGTTGAGGTTGGTCTTTC 1595

RESULT 3
LOCUS AX665980 1546 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02059333.
ACCESSION AX665980
VERSION AX665980.1 GI:29290849
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
REFERENCE 1
AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
TITLE Gene promoters isolated from potato and use thereof
JOURNAL Patent: WO 02059333-A 3 01-AUG-2002;
FEATURES Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:4113"

ORIGIN

Query Match 83.5%; Score 1334.4; DB 6; Length 1546;
Best Local Similarity 93.8%; Pred. No. 1.5e-267;
Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;

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DB 1 ATCTTTGTTGAAAAATTTGAAAGACGCTAGGACCATGACCTTGGTGCACAT 60

QY 109 ATTGTTGCTCTCCAAATGTGTACAGGATTTGTACATCTCCGGGTACTTTAAGCTGAC 168
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61	Db		ATTGTTGCTCTCCAAATGTGGTCAAGAGATTGTTACATCTCCGGGTACTTTAAGCTGAC	120
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121	Db		TAGGACATTCACCATTTATATTGTCGGTCGATTTGAATTTGTGGCATTTCCCTCCACTTG	180
229	Qy		GATTAGTCGGGGCGAAAGTCATCGGTATATTAATATCCATCAATAAAGAAATGTCGAGA	288
181	Db		GATTAGTCGGGGCGAAAGTCATCGGTATATTAATATCCATCAATAAAGAAATGTCGAGA	240
289	Qy		AATCTAAGTTGTTCAACTGCTCCAAAGCGTACTCGGTAGGGTGTGTTGGTGGTTGCCCC	348
241	Db		AATCTAAGTTGTTCAACTGCTCCAAAGCGTACTCGGTAGGGTGTGTTGGCGGTTTACCCC	300
349	Qy		ACCGGTGTCATCGCAGGACACCAACCAATCACCAAGTCATGCACGAACCTCTACCAAGCAC	408
301	Db		ACCGGTGTCATCGCAGGACACCAACCAATCACCAAGTCATGCACGAACCTCTACCAAGCAC	360
409	Qy		CACCGAAGTTACATCCAGTACGACCCCATATATGTCGCATCTAGTGCCTCCTAGGCGCAT	468
361	Db		CATCGAAGTTACATCCAGTACGACCCCATATATGTCGCATCTAGTGCCTCCTAGGCGCAT	420
469	Qy		CAATGACCCACATTTGGCCTCGATCGAGACGTCGGGCACCGCCTATC - GGGTCGATGCCG	527
421	Db		CAATGACCCACGTTTGGCCTCGATCGAGACGTCGGGCACCGCCTATCGGGTTCGATGCTG	480
528	Qy		CCAAACGATGTATGHCACGTTGTTGGCGGTACTCTCGATAGTCAGCAGCATAGTGAAGT	587
481	Db		CCCAGACGGTGTATGGACAGTTGTTG - CGTACCTCGATAGTGGCAGCATAGTGAAGT	538
588	Qy		CACAAAGCCAGAAAGGAGAGAAACAAAGAAAGATCTCAAGTACGCCCATGTTGTTGTAAT	647
539	Db		CACAAAGCAAGAAAGGAGAAACAAAGAAAGATCTCAAGTACGCCCATGTTGTTGTAAT	598
648	Qy		TTATATGTGGACAAATPATTTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCAC	707
599	Db		TTATATGTGGACAAATPATTTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCAC	658
708	Qy		TACGGATATTAAATCGTATTATAAACAATATCATCTTCGACTAAATTTATAAAGCAAAATAT	767
659	Db		TATGGATATTAAATCGTATTATAAACAATATCATCTTCGACTAAATTTATAAACAATPAT	718
768	Qy		ATTACAATATGATTTGGTAAACGTTGAGGTGGAATAATGATATAGGACCGCCCTTAATAAT	827
719	Db		ATTACAATATGATTTGGTAAACGTTGAGGTGGAATAATGATATAGGACCGCCCTTAATAAT	778
828	Qy		AATATTTTATGAATATAGCCTATAGTTACAAGTTAACTTTATTTGGTGTAACTTTGAC	887
779	Db		AATATTTTATGAATATAGACTATAGTTACAAGTGAACTTTATTTGGTGATACTTTGGAC	838
888	Qy		ATATAAACTCTGTAAACGTGACGGAATTTTTCTTTAAAACTAAATATTAAGGACAGACTATT	947
839	Db		ATATAAACTCTGTATCTGTGACGGAACCTTTTCTTTAAAACTAAATATTAAGGACAGACTATT	898
948	Qy		TTCACATTTTTCGTGGCCAAAGTCCTGTGCATCTATCTATATGCCCATTTTTACTTTTAT	1007
899	Db		TTAATATTTTTCGTGGCCAAAGTTCTCTGTGCATCTATCTATGCCCATTTTTACTTTTAT	958
1008	Qy		CGTTCCTAGCCTCTTAGGTACACGTTTGAAACATATAAAATCATAAAAATTCGAAAGTAAAAA	1067
959	Db		CGTTCCTAGCCTCTTAGGTACGCGTTTGAACATATAAAATCATAAAAATTCGAAAGTAAAAA	1018
1068	Qy		TTAGTTTTTTTTTTCATATTACTCGPATGGATCATTTGTTAGATCAATCTGAAATATAC	1127
1019	Db		TTAG - - - TTTTTTTTTCATATTACTCGPATGGATCATTTGTTAGATCAATCTGAAATATAC	1075
1128	Qy		AAACCATCTCGATTTTAAAAATCAACACCATTCGCTTAATGGGGAAGTCTTAT - GTGATTC	1186
1076	Db		AAATCATCTCGATTTTAAAAATCATACATCTATTCGATGATGGGAACGCTCATGGTGATTC	1135
1187	Qy		GTGCGAAGTGTGGA - TTATCTCTTAGTCTAGATTGGAGTCAACAACCTTTTATAGTCAAAATAT	1245

ORIGIN

Query Match 43.2%; Score 689.6; DB 8; Length 2659;
 Best Local Similarity 73.5%; Pred. No. 2.7e-133; Indels 217; Gaps 13;
 Matches 1156; Conservative 0; Mismatches 199;

QY 46 GGTATCTTTGTTGAAAAATTTGAAAAAGACGTAGACACACATCGGCTTGGGTGCAAC 105
 DB 1675 GGCATCTTTTCTTGAATAATTTGGACAACCTCTGTAGGACACATGGACCTTGGGTGCAAC 1616

QY 106 AATATTTGTCCTCCCAATGTGTGACAAAGATTTGTATCATCTCCGGGTACTTTAAGCT 165
 DB 1615 AATATTTGTCCTCCCAACGTGTGACAAAGATTTGTATCATCTCCGGGTACTTTAAGGG 1556

QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCTATGATTTGATTTGCGCATTTCCCTCCAC 225
 DB 1555 CGCGAGGACATTCACCATTTATTTGCGGTGCTATGATTTGATTTGCGCATTTCCAGGAC 1496

QY 226 TTGATTTAGTCGGGCGAAGATTCATCGGTATATTAATPCCATCACTAAAGAAATGTCCT 285
 DB 1495 TAGGTTTGGTCGGGCGAAGATTCATCGGTATATTAATPCCATCACTAAAGAAATATCC 1436

QY 286 AGAATCTAAAGTTGTTGAACGTGTCAGGCGTACTCGGCTAGGCTTTGGTGGTTGC 345
 DB 1435 AGAATCTAGGTTGTTGAACGTGTCAGGCGTACTCGGCTAGGCTTTGGTGGTGGTAC 1376

QY 346 CCCACCGGTGCACTGCAAGACTCCACCAATCACCAGTCAATGACGAACTCTAGCAG 405
 DB 1375 CCCACCGGTGCACTGCAAGACTCCACCAATCACCAGTCTGACACGAACTCTAGCAG 1316

QY 406 CACGACCAAGTTATCATCTGACGACGACGACGACGACGACGACGACGACGACGACG 465
 DB 1315 CAGCATTAAGTTTCAACGACGACGACGACGACGACGACGACGACGACGACGACG 1256

QY 466 CATCAATGACCACTTTGGCTCGATCGACGACGACGACGACGACGACGACGACGACG 524
 DB 1255 CATGATGACCCATTTGGCTCGATCGACGACGACGACGACGACGACGACGACGACG 1196

QY 525 CGGCCAAACGATGATGCAAGTTTGGCGGTACCTCGATGATGACGACGACGACGACG 594
 DB 1195 CTGCCCAACGATGATGCAAGTTTGGCGGTACCTCGATGATGACGACGACGACGACG 1138

QY 595 AGTCACAAAGCCGAGAGGAGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
 DB 1137 AGTCACAAAGCCGAGAGAGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078

QY 641 TTGAAATTTATATGTGCAAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTT 700
 DB 1077 TTGAAATTTATATGTGCAAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTT 1019

QY 701 TTGGCACTACGATATTAAT---CGTATATATACAAATATCATCTTTGACTTAATATA 757
 DB 1018 TTGGCACTACGATATTAAT---CGTATATATACAAATATCATCTTTGACTTAATATA 959

QY 758 AACGAAATATATACAAATATGATTTGGTAAACGTTGAGGTGAAATATGATAGAGCG 817
 DB 958 AACGAAATATATACAAATATGATTTGGTAAACGTTGAGGTGAAATATGATAGAGCG 911

QY 818 CCTAATAATTAATTTTATGATATAGCCTATAGTTACAGTTAACTTTATTTGGTGA 877
 DB 910 CCTAATAATTAATTTTATGATATAGCCTATAGTTACAGTTAACTTTATTTGGTGA 889

QY 878 TAACTTTGACATATAAATCTGTACGAGCGGATTTTCTTAAACATTAATATT--- 933
 DB 888 TAACTTTGACATATAAATCTGTACGAGCGGATTTTCTTAAACATTAATATT--- 844

QY 934 ---AAAAAGCAGCTATTTTCACTTTTTCGTCGCAAGAGTCTTGTGACATCTTATGATG 990
 DB 843 TAAAAAAAAGCAGCTATTTTCACTTTTTCGTCGCAAGAGTCTTGTGACATCTTATGATG 784

QY 991 CCCATTTTATCTTTATCGTTCTAGCTTCTAGGTACAGGTTTGAACATATAAATAATATA 1050
 DB 783 CTCATTTT---TACITTTTATCGTTTGTAGTACGCAATTTGAACATATAAATAATATA 733

QY 1051 ABAATGGAAGTAAATAATAGTTTATTTTTCATATTACTC---CTATGATCATTTGT 1107
 DB 732 ABAATGGAAGTAAATAATAGTTTATTTTTCATATTACTCGTAGTATGATCATTTGC 673

QY 1108 TAGATCAATCTGAAATATACAAACCATTTCTGATTTTAAATACAAACCATTTCTGCCTAAT 1167
 DB 672 TAGATTAACATGAATATACAAATCAACGATTTTGTATGATGACAGATCATTTG--- 619

QY 1168 GGGGAAGTCTATGTGATTCGTGCAAGTGTGTGATTTATTTCTTAGTCTAGATGGAGTCA 1227
 DB 618 -----TTGACCAACA 609

QY 1228 AACTTTTAGTGCAAAATATCTATTATAAGAACCCCTATTGATGCAAAATATCTATAAAGA 1287
 DB 608 ACTTTTAAATGCAAGTATCTATTATAAGAACCCCTATTGATGCAAAATCAAT--- 556

QY 1288 ACCCTATTTCATCTATTATTTATTTTACGATCGGAGCATGATATATTACTTAATAA 1347
 DB 555 -----AA 554

QY 1348 ATAAATTTGGAGGAATTTGATCGACAGCCATCAAGCTTATCGTCGATCCACATTAGGATA 1407
 DB 553 ATAAATTTGGAGGAGTGTGATGCAAGTCTCAAACTTATCGTCGATCCACATTAAATA 494

QY 1408 ACCTTAGTATGGCTGTTTTAGAGAAACAAAGTGGATCATGTACAAATTTGAGTT-AAAAAT 1466
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QY 1467 ATCTCTATAAATACCTGTCTATCCCTCTTAAACCAATACATCTAACACACAAATATA 1526
 DB 433 ATCTCTATAAATATATATCTATCTCTCTTAAACCAATACATCTAACACACAAATATA 374

QY 1527 AACTTAGATTTCTTAAAGAAATTTGAGAATTTAAATGGAGGCAAAATAGTCTATGTTGAAG 1586
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QY 1587 TTGGTTGCTTTTC 1598
 DB 313 TTGGTTGCTTTTC 302

RESULT 5
 SC130LP/c
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 DEFINITION S.commerstonii (posML13) gene for osmotin-like protein.
 ACCESSION X72928
 VERSION X72928.1 GI:296771
 KEYWORDS osmotin-like protein,
 SOURCE Solanum commerstonii (Commerston's wild potato)
 ORGANISM Solanum commerstonii

REFERENCE
 1. Zhu, B., Chen, T. H. and Li, P. H.
 Activation of two osmotin-like protein genes by abiotic stimuli and
 fungal pathogen in transgenic potato plants
 JOURNAL Plant Physiol. 108 (3), 929-937 (1995)
 MEDLINE 95357444
 PUBMED 7630973

REFERENCE
 2. (bases 1 to 2638)
 AUTHORS Zhu, B.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
 Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
 COMMENT Related sequences: M29279 & M21346.
 FEATURES Location/Qualifiers
 1. .2638
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ORIGIN
Query Match 33.3%; Score 531.4; DB 8; Length 2638;
Best Local Similarity 76.1%; Pred. No. 2.4e-100; Indels 28; Gaps 5;
Matches 730; Conservative 0; Mismatches 201;

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Db |||
QY 1983 GGCATCTTTGTTGGAAGATCTTGACAAGTCAGTAGGACCACATGGACCTTGGGTGCAAC 1924
Db |||
QY 106 AATATTGTTGTCCTCCAAATGCTGACAGGATGTTACATCTCCGGGTACTTTAAGCT 165
Db |||
QY 1923 AATATTGTTGTCCTCCGAACTGTTGACAGGATGTTACATCTCCAGGTACCTTAAGT 1864
Db |||
QY 166 GACTAGGACATTCACCATTTATATTTGCCGTCGATTCGAATGTTGTCGATTTCCCTCCAC 225
Db |||
QY 1863 AACGAGACATTCACCATTTATATTAGCCGTGCAATGAATTCGTCGCAATTCCTCCAC 1804
QY 226 TTGAATTAGTCGGGGCGAAGTCATCGGTATATTAAATTCATCAATCAAGAAATGTCCC 285
Db |||
QY 1803 TAGGATTAGTTGGGGCGAAGTCATCGGAATATTAAATTCATCAAGAAATGTCCC 1744
QY 286 AGAATCTTAAGTTGTAACCTGGTCCAAAGGCGTACTCGGTAGGCTGTTTGGTGGTTTC 345
Db |||
QY 1743 AGAATCTAGTTGCTGNACTGGTCCAAAGGCGTACTCGGCAGGGTGTGTTGGTTTC 1684
QY 346 CCCACCCGGTGCATCGAGGACACACACAAATCACCACTGATCGACGAACCTCTACCA 405
Db |||
QY 1683 CCCACCCGGTGCATCGAAGACCCACCAATCACCACTGATCGACGAACCTCTACCA 1624
QY 406 CACCACCGAAGTTACATCCAGTACGCCCATATACGTGCGCATCGTAGTCCCTAGGCG 465
Db |||
QY 1623 CACCATCAAGTTGCAATTAGTAGCAGCCCATATACGTGCGCATCTTAGTCCCTTAGGCG 1564
QY 466 CATCAATGACCCATTTGGCTCGATCGAGACGTGGGACCGCCCTATC- GGGTCCATG 524
Db |||
QY 1563 CATGTAAACCCATGTCTGGCTCGATCAAGACGTGGGCCACCGCTCTCGGGTGCATG 1504
QY 525 CCGCCCAACGATGTATGACAGTTGTTGGGTACCTCCATAGTAGACACATAGTGAA 584
Db |||
QY 1503 CCGCCCAACGTTGATGGACAGTTATG--CGTACCTCATAGTGGCAGCATAGTGTA 1446
QY 585 AGTCACAAAAGCCAGAGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTGTTGA 644
Db |||
QY 1445 AGTCACAAAAGCCAGAGAGGAGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTGTTGA 1386
QY 645 AATTATATGTGGACAAATTTATTTTGGTA-----CTTTATATATAG 686
Db |||
QY 1385 ACTATATATTTTAACTAAGTTGTTTGATATTGTGACAAATTTGTGGCGAGTTATATAG 1326
QY 687 GGATATCGCGCTTTTGGCACTAGGATATTAACTCGTATTATATACAAATATCATACTTT 746
Db |||
QY 1325 GGGTGTGGCGCTTTTGAACACTAGGATTTTATC---ACAAATATCAATATCACACTT- 1270
QY 747 GACTAAATTAAACGAATATTATTAATATGATTGGTAAACGTTGAGGTGGAATAATG 806
Db |||

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1269 ---GACTAATCAACGCATAATATTGAAATATGTTTAACTAAGTTGAGCGGCTCAACA 1213

807 TATAAGAGCGCCTAATAATTAATTTATTTATGAAATATAGCTTAGTCAAGTAACT 866

1212 TATAAGAGCGCCTACTAATAATTTACTCCATAACTTTTATATAGTCAAACTATTATTTATT 1153

867 TTATTGTTGATAAAGCTTTGACATATAAACTCTGTAACTGACGGAATTTTCTTAAACT 926

1152 TGATTCTTATCTAGTGTTCGATATATGTTCTGTTTAAATCTTAATTTACAAATTA 1093

927 AAATATTTAAAGACGAGCTATTTCACATTTTTCGTCGCAAAAGTCTCTTGCACTAT 985

1092 TAGTGTCTTAAAGATTTTTCATTTCTAAAGATTCAAATTCACATTTGATTAGAA 1034

RESULT 6

AF093743/c

LOCUS

DEFINITION

Lycopersicon esculentum pathogenesis-related protein osmotin

precursor (NP24) gene, complete cds.

ACCESSION

AF093743

VERSION

AF093743.1 GI:3747059

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

REFERENCE

1 (bases 1 to 1304)

Jia,Y. and Martin,G.B.

REFERENCE

AUTHORS

Jia,Y. and Martin,G.B.

TITLE

Rapid transcript accumulation of pathogenesis-related genes during an incompatible interaction in bacterial speck disease-resistant tomato plants

JOURNAL

Plant Mol. Biol. 40 (3), 455-465 (1999)

MEDLINE

99364540

PubMed

10437829

REFERENCE

2 (bases 1 to 1304)

Martin,G.B. and Jia,Y.

AUTHORS

Martin,G.B. and Jia,Y.

TITLE

Direct Submission

JOURNAL

Submitted (22-SEP-1998) Boyce Thompson Institute, Tower Road, Ithaca, NY 14853-1801, USA

FEATURES

Location/Qualifiers

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/cultivar="Ailsa Craig"

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ORIGIN

Query Match 32.9%; Score 525.8; DB 8; Length 1304;

Best Local Similarity 78.3%; Pred. No. 3.5e-99;

Matches 710; Conservative 0; Mismatches 182; Indels 15; Gaps 6;

QY 49 ATCTTTGTTTGAATAAATTTGGAAGACGCTAGGACCACTGGACCTTGGTGCACAAAT 108

Db |||

912 ATCTTTTCTTGAATAAATTTGGAACAACTCTGAGGGCCACATGGACCTTGGGTGCACAAAT 853

Qy	109	ATTGTTGCTCCTCCAAATGTGGTGA	CAAGGATTGTTTACATCTCTCGGGTACTTTAAAGTCGAC	168
Db	852	ATTGTTGCTCCTCCAAACGTGGTAC	AAGGGTGTGTTTACATCTCTCAGGTACCTTAAAGGGCGC	793
Qy	169	TAGGACATTACACATTTATTTGTC	CGTGCAATCGAATTTGGTGGCATTTCCCTCCACTG	228
Db	792	GAGGACATTACACATTTATTTGTC	CGTGCAATCGAATTTGGTGGCATTTCTTCTCACTAG	733
Qy	229	GAATTAGTCGGGCGGAAAGTCAT	TCGGTATATTAAATCCATCAACTAAAGAAATGTC	288
Db	732	GTTTGTTCGGGCGGAAAGTCAT	TGGGAATATTAAATCCATCGACTAAGAAATGTC	673
Qy	289	AATCTAAGTGTGTTGAACCTGGT	CCAGGGGTACTCGGCTAGGCTGTTTGGTGGTTTGG	348
Db	672	AATCTAAGTGTGTTGAACCTGGT	CCAGGGGTACTCGGCTAGGCTGTTTGGGGGTTTGGCC	613
Qy	349	ACCCGCTGCACTGCAGGACAC	CCACCAATCACCAAGTCATGCACGAACCTCTAC	408
Db	612	ATCCGCTACACTGTAAGACTCC	ACCACCAATCACCAAGTCATGCCTTGCCTGCAG	553
Qy	409	CACCGAAGTTACATCCAGTAC	GCACCCCATATACGTGCATCTGTAGTGCCTTAG	468
Db	552	CATTAAAGTTGCAACAGTAG	CAACCCCATATACGTGCATCTTAGTTCCCTCG	493
Qy	469	CAATGACCCACATTTTGGCTCG	ATCGACATCGCGCACCGCCTATCGG-GT	527
Db	492	TGATGACCCATGTTTGGCTCG	ATTGAGACGTGCACACCGCCTATCGGATCG	433
Qy	528	CCGAAACGATGTATGCAAGTT	TGTGGCGGTACCTCGATAGTGACAGCATPA	587
Db	432	CCCAACCGGTGTATGGACAG	TTGTTGC--GTACCTCAATAGTGGCAGCAT	375
Qy	588	CACAAAGCCGACAGGGAGAAC	CAAAAGAGATCTCAAGTAGCCCATGTTTGTG	647
Db	374	CACACAAAGAGAGAGAGAA	GCATCAAGTAGCCCATGTTTGTGGAAT	315
Qy	648	TTATATGTGACAAATATTTTGG	TATA-CTTTATATATAGGATATGGCGCTTT	706
Db	314	GTATATATGAGGATAACTTAT	TGAAAGCACTTTATATAGGGGTGTGGCG	255
Qy	707	CTACCGATTAATCGTATTAT	TAACCAATATCATCTTTGCACTAATTATA	766
Db	254	CTATGTATATTATTC--AT	AAATTAACCAATATCATATTTGACAAAAA	198
Qy	767	TATTACAATATGATTGGTAA	ACGTT-TCGAGGTGAAAAATGTTATAAG	825
Db	197	AAATACGATATAGTAAAGT	GAGGTTGAAAAAGAAAAATGTATAAG	138
Qy	826	TTAATTTATTTAATATAG	CTTATAGCTATAGTACAGTTTAACTTTAT	885
Db	137	ATAATAATTTTATCAA-----	ATATAGTACAAAGTTTCACTTTATTTCT	85
Qy	886	ACATATAAACTCTGTAA	CGTGACGGAATTTTTTCTTAAAACTAA	945
Db	84	TAACGTGACGGAACTTAT	TTCTCAAAATAATATATTTAAAAA	25
Qy	946	TTTTTCAC	952	
Db	24	TGCTGAC	18	

RESULT 7	SCOSMLP/c	LOCUS	SCOSMLP	901 bp	mRNA	linear	PLN 16-MAR-1993
DEFINITION	S. commersonii mRNA for osmotin-like protein.						
ACCESSION	X67121						
VERSION	X67121.1 GI:21194						
KEYWORDS	osmotin-like protein.						
SOURCE	Solanum commersonii (Commerson's wild potato)						
ORGANISM	Solanum commersonii						
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.						

REFERENCE 1 (bases 1 to 901)
AUTHORS Zhu,B., Chen,T.H. and Li,P.H.
TITLE Expression of an ABA-responsive osmotin-like gene during the induction of freezing tolerance in *Solanum commersonii*
JOURNAL Plant Mol. Biol. 21 (4), 729-735 (1993)
MEDLINE 93192535
PubMed 8448373
REFERENCE 2 (bases 1 to 901)
AUTHORS Zhu,B.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1992) B. Zhu, Dept of Horticulture, AG & Life Science 4017, Oregon State University, Corvallis OR 97331, USA
FEATURES Location/Qualifiers
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 Best Local Similarity 89.4%; Pred. No. 4.2e-89;
 Matches 537; Conservative 0; Mismatches 61; Indels 3; Gaps 2;

 46 GGTATCTTCTTTGAAAAATTCGAAAGAACTAGGACCACATGGACCTGGGTGCAAC 105
 Db GGCATCTTTGTTGAAGATCTTGAACGTCAGTAGACCAATGGACCTGGGTGCAAC 550

 106 AATATTGTTGTCCTCAAATGTGGTCAAGGATTGTATACCTCCGGGTACTTTAAGCT 165
 Db AATATTGTTGTCCTCGAACGTGGTCAAGGATTGTATACCTCCAGGTACCTAAGT 490

 166 GACTAGACACATCACCATTATATTTGCCGTGATGAATGTGTGCAATTCCTCCAC 225
 Db AACAGACACATCACCATTATATATGACCGTGAATGAATGGTGGCATTTCCCTCC 430

 226 TTGGATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCCC 285
 Db TAGGATTAGTTGGGGCGAAGTCATCGGAATATTAAATCCATCGACTAAAGAAATGTCCC 370

 286 AGAAATCTAAGTTGTTGAATCGTGCAGCGGTACTCGGGTAGGGTGTTTGGTGGTTGC 345
 Db AGAAATCTAGGTTGCTGAACTGTGTCCAAAGCGGTACTCGGGCAGGGTGTTTGGTGGTTGC 310

 346 CCACCCGGGTGCACTGCAGGACACCAACAATCACCAGTCATGCACGAACCTCTACCAG 405
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 406 CACCAACGAAGTTACATCCAGTACGACCCCAATATACGTGCGATCGTAGTGCCTTAGCG 465
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 466 CATCAATGACCCACATTTGSCCTCGATCGAGAGCGTCGGGACCCGCTATC-GGGTCGATG 524
 Db CATTGATPACCCATGTCGTGGCCTCGATCAAGAGCGTCGGCCACCGCTATCGGGGTGATG 130

 525 CCGCCCAACGATGTATGGACAGTTGTTGGCGGTACTCTCGATAGTGACACATAAGTGAA 584

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Db      129  CCGCCCAACACGGGTATGGACAGTTGTG--CGTACCTCGATAGTGGCAGCAATAAGTGTA 72
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Db      71   AGTCACAAAGCCAGAGAGGAGAGAGAGAGATCTCAAGTAGCCCATGTTTGTGGA 12
Qy      645  A 645
Db      11   A 11

RESULT 8
NTOSPR/c
LOCUS   NTOSPR N.tabacum osmotin gene. 2033 bp DNA linear PLN 01-FEB-1996
DEFINITION
ACCESSION X95308
VERSION X95308.1 GI:1167853
KEYWORDS osmotin; PR protein.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Barnard,W.M. and Neale,A.D.
TITLE Comparison of the 5 regulatory regions of homeologous osmotin genes from Nicotiana tabacum
JOURNAL Unpublished
AUTHORS Neale,A.D.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1996) A.D. Neale, Monash University, Genetics and Developmental Biology, Wellington Rd, Clayton, Victoria, 3168, Australia

FEATURES
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ORIGIN
Query Match 29.4%; Score 469.2; DB 8; Length 2033;
Best Local Similarity 75.3%; Pred. No. 2.1e-87;
Matches 661; Conservative 0; Mismatches 188; Indels 29; Gaps 5;

Qy      46   GGTATCTTTGTTCAAAAATTTGAAAGAACGTPAGGACCACATGGACCTTGGGTGCAAC 105
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Qy      106  AATATCTTGTCTCCAAATGTGGTACAAGATGTTGTACATCTCCGGGTACTTTAAGCT 165
Db      1685  AATATTGTTGTCCTCCAAATGTAGTACAAGGGTTATTACATCTCTCCGGGAACCTAAGTT 1626

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Qy      166  GACTAGGACATTCACCATTTATTTTGGCGTCATTTGAATTTGTGTGGCATTTCCCTCCAC 225
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Qy      226  TTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGCCCC 285
Db      1565  TAGGGTTAGTCGGGGCGAAAGTCATCGGTATGTTGAATCCATCTACTAAGAAATGCCCC 1506
Qy      286  AGAAATCTAAGTTGTGAACCTGGTCCAAAGGCGTACTCGGCTAGGGTGTGGTGGTTGC 345
Db      1505  AAAATCTAAGCCACTGAATTTGGTCCATGCTATTGGCCCAAGGTGTTTGGTGGTTTAC 1446
Qy      346  CCCACCCCGTGCATGACGAGCACCACCAATCACCAGTCATGCAGCAACCTCTACCAG 405
Db      1445  CCCACCCCGTGCATTTGTAGGACTCCACCAAGTCACCGGTTTGGCATGTACCCCTACCAG 1386
Qy      406  CACCACCGAAGTTACATCCAGTACGACCCCATATACGTCGTCATGTCCTCCCTAGGCG 465
Db      1385  CAGCATTAAGTTACAAATTTGTACGACCCCATATAAGTGCCATTTAGTACTCTGTGGCG 1326
Qy      466  CATCAATGACCCACATTTGGGCTCGATCGAGAGCTCGGGGACCCGCTAT--CGGTCGATG 524
Db      1325  CATTCATCACCCCAAGTTTGGGCTCGATCGAGGCGTCGGCCACCCGCTATGGGGGTGCAAG 1266
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Db      1265  CGGCCCAACCGTGTACGGGCAAGTTGTT--TCGACCTCGATAGTTGCGAGCATTAAGTACA 1208
Qy      585  AGTCACAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGTA 644
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Qy      645  AATTATATGTGGCAAAATTTTTCGTACTTATATATAGGATAGGGGATGGCGGCTTTT-- 702
Db      1147  CATTTCTTTTAAACAAGTTGCGTTGTTGGATATAGTGAACAAATTTTGTGGTTTATAT 1088
Qy      703  -----GGCACTACGGATATTAATCGTATTATATATAAATAATCATATCTTGTACTA 751
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Qy      752  ATTATAACGAAATATATATCAATATGATTTGGTAAAGCTTGAGTGGGAAATATATAA 811
Db      1027  CTAGTAAATGGAATATCTCAAGGATGCTTTAGTAAAGGTGAGCGCGCTAAAAAGTATAA 968
Qy      812  GAGCGCGCTAAT--AATTAATTTTATGAATATAGCCTATAGTTACAAAGTTAACTTTAT 870
Db      967  GAGCGCGCTAATTAACATAATTTTATGATATAG-----AAGTCAATTTAT 920
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Db      919  TTGGTGATGCTGACCTGACCTATAAGCTCTGTAAACGTGAC 882

RESULT 9
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LOCUS   N.tabacum ap24 gene.
DEFINITION X65701
ACCESSION X65701.1
VERSION X65701.1
KEYWORDS osmotin.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Melchers,L.S., Sela-Buurlage,M.B., Vloemans,S.A., Woloshuk,C.P., Van Roessel,J.S., Pep,J., van den Elzen,P.J. and Cornelissen,B.J.
TITLE Extracellular targeting of the vacuolar tobacco proteins AP24, chitinase and beta-1,3-glucanase in transgenic plants
JOURNAL Plant Mol. Biol. 21 (4), 583-593 (1993)
MEDLINE 93192519

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PUBMED 8448358
 REFERENCE 2 (bases 1 to 1549)
 AUTHORS Melchers, L.S.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-1992) L.S. Melchers, Mogen International NV,
 Einsteinweg 97, 2333 CB Leiden, THE NETHERLANDS
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 Best Local Similarity 76.8%; Pred. No. 2.6e-87;
 Matches 679; Conservative 0; Mismatches 162; Indels 43; Gaps 7;
 QY 46 GGTATCTTGTGTAAGAAATGGAAAGACGTAGGACACATGGACCTTGGGTGCAAC 105
 DB 1027 GGCATCTTGTGTAAGAAATTTGAGAAAATGAGGACCAAGGCTTGTGTGCAAC 968
 QY 106 AATATTTGTCTCCCAATGTGTGATCAAGGATTTTACATCTCCCGGTACTTTAAGCT 165
 DB 967 AATATTTGTCTCCCAATGTGTGATCAAGGATTTTACATCTCCCGGTACTTTAAGCT 908
 QY 166 GACTAGGACATTCACCATTTATTTGGCGTGCATTTGAATTTGTGGCATTTCCCTCCAC 225
 DB 907 CGCGGGGACATTCGCGGTTTATTTAGCCGTACCAATGAATTTGCATTTCCCTCCAC 848
 QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCCC 285
 DB 847 TAGGTTAGTCGGGGCGAAAGTCATCGGTATTTGAATTCATCACTAAGAAATGTCCC 788
 QY 286 AGAATCTAAGTTGTGTGAACCTGGTCCAAAGCGGTACTCGGCTAGGCTTTGGTGTTCG 345
 DB 787 AGAATCTAAGTTGTGTGAACCTGGTCCAAAGCGGTACTCGGCTAGGCTTTGGTGTTCG 728

QY 346 CCCACCGGTGCACTGCGAGGACACCAACCAATCAACAGTCAATGACGACCACTTCTACCAG 405
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 QY 406 CACACCGGAAGTTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCG 465
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 DB 257 AACATAAGAGCGCCCTAATAATTAATTTATTTATGAATATAG-----AAGTCA 210
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 DEFINITION Sequence 1 from patent US 5801028.
 ACCESSION AR037158
 VERSION AR037158.1 GI:5955014
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 3033)
 Bressan, R. and Hasegawa, P.M.
 TITLE Osmotin gene promoter and use thereof
 JOURNAL Patent: US 5801028-A 1 01-SEP-1998;
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 Best Local Similarity 76.8%; Pred. No. 2.6e-87;
 Matches 679; Conservative 0; Mismatches 162; Indels 43; Gaps 7;
 QY 46 GGTATCTTGTGTAAGAAATTTGAGAAAATGAGGACCAATGGACCTTGGGTGCAAC 105
 DB 2622 GGCATCTTGTGTAAGAAATTTTGAAGAAAATGAGGACCAAGCTCTTGTGTGCAAC 2563
 QY 106 AATATTTGTCTCTCCAAATGTGTGTAACAGGATTTTACATCTCCCGGTACTTTAAGCT 165
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Qy      865  CTTTATTTGGTGATACCTTTGACATATATAAACTGTGTACGTGAC 908
Db      1804  ATTATTTGGTAATAACCTGACCTATTAATCTCTGTAAAGTGAC 1761

RESULT 12
AF473702/c
LOCUS   Solanum nigrum osmotin-like protein gene, complete cds.
DEFINITION
ACCESSION AF473702
VERSION   AF473702.1 GI:19874518
KEYWORDS
SOURCE   Solanum nigrum (black nightshade)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS   Jaml,S.K. and Kirti,P.B.
TITLE     PCR-based cloning of an osmotin-like protein gene from Solanum
nigrum
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 729)
AUTHORS   Jaml,S.K. and Kirti,P.B.
TITLE     Direct Submission
JOURNAL   Submitted (21-JAN-2002) Department of Plant Sciences, University of
Hyderabad, Gachibowli, Hyderabad, A.P 500046, India
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ORIGIN
Query Match 28.1%; Score 449.8; DB 8; Length 729;
Best Local Similarity 87.3%; Pred No 2.4e-83;
Matches 516; Conservative 0; Mismatches 72; Indels 3; Gaps 2;

Qy      46  GGTATCTTTGTTGAAAAAATGGAAGAACGTTAGGACCAATGAGCCTTGGGTGCAAC 105
Db      589  GGCATCTTTGTTGAAAAAATTTGACAATTCGGTAGGACCAATGAGCCTTGGGTGCAAC 530
Qy      106  ATATATGTTGCTCCTCAATGTTGACAGGATTTGATCATCTCCGGTACTTTAAGCT 165
Db      529  AATATTGTTGCTCCTCGAACGGTGACAGGATTTGATCATCTCCGGTACTTTAAGTG 470
Qy      166  GACTAGGACATTCACCAATTATATTGTCGCGTCAATGAATTTGTGGCATTTCCCTCCAC 225
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Db      469  CAGCAGGACATTCACCATTTATATTATTTGGCGGTGCATTTGAATTCAGTGACATTTCCCTCCAC 410
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Qy      286  AGAAATCTAAGTTGTTGAACTGGTCCAAAGCGGTACTTCGGCTAGGGTGTGTTGGTGGTTGC 345
Db      349  AGAAATCTAGATTGCTGAACTGATTCAAAGCGTATTTCCGCTAGGGTGTGTTGGGGGTTTC 290
Qy      346  CCACCCGGTGCTACCTCAGGACACCAACATCACCAGTATCGACGACCACTTACCCAG 405
Db      289  CCACCCGGTACACTCAGGACCCCAACCAATCACCAGTCTGGCATGAACCTTCTACCAG 230
Qy      406  CACCACCGAAGTTACATCCAGTACGACCCCAATATAGTCCCATCGTAGTGCCTTAGGGG 465
Db      229  CACATCGAAGTTGCAATTAGTAGACCCCATATAGTGCCTACTAGTGCCTTGGTG 170
Qy      466  CATCAATGACCCACATTTGGCCCTCGATCGAGACGTGGGCGACCGCTATC-GGGTCGATG 524
Db      169  CATTGATGACCCATGTCTGCGCTCGATCGAGACGTGACCCACCGCTATTCGGGGTTCGACG 110
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RESULT 13
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LOCUS   Lycopersicon esculentum PR-5x (PR-5) mRNA, complete cds.
DEFINITION
ACCESSION AY093595
VERSION   AY093595.1 GI:20750096
KEYWORDS
SOURCE   Lycopersicon esculentum (tomato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 917)
Rep,M., Dekker,H.L., Vossen,J.H., De Boer,A.D., Houterman,P.M.,
Speijer,D., Back,J.W., De Koster,C.G. and Cornelissen,B.J.C.
Mass Spectrometric Identification of Isoforms of PR Proteins in
Xylem Sap of Fungus-Infected Tomato
Plant Physiol. 130 (2), 904-917 (2002)
22264016
12376655
2 (bases 1 to 917)
Rep,M., Dekker,H., Vossen,J.H., de Boer,A., Houterman,P.,
Speijer,D., Back,J.-W. and Cornelissen,B.J.C.
Direct Submission
Submitted (28-NOV-2002) Plant Pathology, University of Amsterdam,
Kruislaan 318, Amsterdam 1098SM, Netherlands
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Best Local Similarity 85.7%; Pred. No. 2.6e-83;
Matches 523; Conservative 0; Mismatches 84; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAGACGTAGGACCACTGGACCTTGGGTGCAAC 105
DB 608 GGCACCTTTGTTGAAAAATCTCGAAAATTTGTAGGACCACTGGGCTTGGTACAA 549
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DB 548 AATATTGTTGCTCCTCGAACGTGTACAAAGGTTGTTACATCTCCGGGTACCTTAAGT 489
QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATGAATTTGTGTGGCATTTCCCTCCAC 225
DB 488 GACTAGGACATTCACCGTTTATTTAGCGGTGCAATGAATTTGTCATGTCATTTTCCCTCCAC 429
QY 226 TTGGATTAGTGGGCGGAAAGTCATCGGTATATTAATTAATCCATCACTAAGAAATGTCCT 285
DB 428 TAGGATTGTTGGGCGGAAAGTCATCGGTATATTAATTAATCCATCACTAAGAAATGTCCT 369
QY 286 AGAAATCTAAGTTGTGAATCGTCCAGGCGTACTCGGCTAGGCGTGTGGTGTGCTTTC 345
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DB 188 CATTCATGACCCCATTTGGCTCGATCGAGACGTCGGGACGCGCTATC-GGGTCGATG 129
QY 525 CCGCCCAACGATGTATGGACGATTTGGCGGTACCTCGATAGTACGATAGTACGATAGTAA 584
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QY 585 AGTCACAAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGGCCCATGTTTGTGA 644
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QY 645 AATTTATATG 654
DB 10 CATATTTTGG 1

RESULT 14
AF450276/c
LOCUS
DEFINITION Solanum nigrum osmotin-like protein precursor (Olp) gene, complete cds.
ACCESSION AF450276
VERSION AF450276.1 GI:19401630
KEYWORDS
SOURCE Solanum nigrum (black nightshade)
ORGANISM Solanum nigrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 744)
Campos,M.A., Ribeiro,S.G., Rigden,D.J., Monte,D.C. and Grossi de
Sa,M.F.
TITLE Pathogenesis related-like genes of Solanum nigrum: cloning and
characterization of genes coding for neutral and basic PR5-like
proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 744)
AUTHORS Campos,M.A., Ribeiro,S.G., Monte,D.C. and Grossi de Sa,M.F.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2001) PBI, Embrapa Genetic Resources and
Biotechnology, P.O. Box 02372, Brasilia, DF 70770-900, Brazil
FEATURES
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Query Match      28.1%; Score 449.4; DB 8; Length 744;
Best Local Similarity 87.1%; Pred. No. 2.9e-83;
Matches 515; Conservative 1; Mismatches 72; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATGGAAAAGACGTAGGACCACTGGACCTTGGGTGCAAC 105
DB 589 GGCATCTTTGTTGAAAAAATTTGACAATTCGAGGACCACTGGGTTGGGTGCAAC 530
QY 106 AATATTGTTGCTCCTCAAAATGTGGTACAAAGATTGTTACATCTCCGGGTACTTTAAGCT 165
DB 529 AATATTGTTGCTCCTCGAACGTTGTACAAAGATTGTTACATCTCCGGGTACTTTAAGT 470
QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATGAATTTGTGTGGCATTTCCCTCCAC 225
DB 469 CAGCAGGACATTCACCATTTATTTGCGCGTGCATTTGAATTTGAGTGAATTTCCCTCCAC 410
QY 226 TTGGATTAGTGGGCGGAAAGTCATCGGTATATTAATTAATCCATCACTAAGAAATGTCCT 285
DB 409 TAGGATTGTTGGGCGGAAAGTCATTTGGAATTAATTAATCCATCGACTAATGATATGTCCT 350
QY 286 AGAAATCTAAGTTGTGAATCGTGGTCCAAAGGCGTACTCGGCTAGGCGTGTGGTGGTTTC 345
DB 349 AGAAATCTAAGTTGTGAATCGTGGTCCAAAGGCGTATTGGGCTAGGCGTGTGGTGGGTTTC 290
QY 346 CCCACCGGTGCTAGGACGACACCAACATCAGATCAGATCAGATCAGATCAGATCAGAT 405
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DB 229 CACCATCGAAGTTGCAATTTAGTACGACGACGACGACGACGACGACGACGACGACG 170
QY 466 CATCAATGACCCCATTTGGCTCGATCGAGACGTCGGGACGCGCTATC-GGGTCGATG 524
DB 169 CATTCATGACCCCATTTGGCTCGATCGAGACGTCGGGACGCGCTATC-GGGTCGATG 110

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QY	525	CCGCCCAACGATGTATGGACAGTTGTTGGCGGTACTCTCATATAGTATGACACGATAAGTGAA	584
Db	109	CCGCCCAACGATGTATGGACAGTTGTT--TCGGACCTCGAAAGAGGTAGCATAAAGTATA	52
QY	585	AGTCACAAAAGCCAGAGGAGAGAACCAAAAGAGATCTCAAGTAGCCCAT	635
Db	51	AGTCACAAAAGTAAAGGAGAGAAACAAAGAGATCTCAGTAGCCCAT	1
RESULT 15	AY007309/c	818 bp	linear
LOCUS	AY007309	818 bp	linear
DEFINITION	Solanum dulcamara cryoprotective osmotin-like protein mRNA, complete cds.		
ACCESSION	AY007309		
VERSION	AY007309.1	GI:10445202	
KEYWORDS			
SOURCE	Solanum dulcamara		
ORGANISM	Solanum dulcamara		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; famids; Solanales; Solanaceae; Solanum.		
AUTHORS	1 (bases 1 to 818)		
TITLE	Newton, S.S. and Duman, J.G.		
JOURNAL	An osmotin-like cryoprotective protein from the bittersweet nightshade Solanum dulcamara		
MEDLINE	Plant Mol. Biol. 44 (5), 581-589 (2000)		
PUBMED	21033368		
REFERENCE	11198420		
AUTHORS	2 (bases 1 to 818)		
TITLE	Newton, S.S. and Duman, J.G.		
JOURNAL	Direct Submission		
FEATURES	Submitted (23-AUG-2000) Biological Sciences, University of Notre Dame, Galvin Life Sciences Bldg., Notre Dame, IN 46556, USA		
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ORIGIN			
Query Match	28.1%	Score 448.4;	DB 8; Length 818;
Best Local Similarity	86.6%	Pred. No. 4.6e-83;	
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QY	166	GACTAGACATTCACCATTTATATTTCGGTGCATTTGAATTGTGTGGCATTTCCCTCCAC	225
Db	490	AACAGGACATTCACCATTTATGTTAGTCGGTGCATTAATGATGTCATGCAATTTCTCTCCAC	431
QY	226	TTGGAATTAGTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTC	285
Db	430	TAGATTGTCGGGCGGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTC	371
QY	286	AGAAATCTAAGTTGTTGAACCTGCTCCAAAGCGTACTCGGTAGGCTGTTGGTGGTTTGC	345

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:32:09 ; Search time 571.22 Seconds
(without alignments)
11884.422 Million cell updates/sec

Title: US-10-051-307-2

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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9: Geneseqn2003cs.*
10: Geneseqn2004s.*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1596.4	99.9	1598	6	ABX90561	Abt90561	Potato pr
2	1480.6	92.7	1595	6	ABX90560	Abt90560	Potato pr
3	1344	84.1	1546	6	ABX90562	Potato pr	
C 4	468.8	29.3	3033	2	AAV52754	Nicotiana	
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C 6	419.8	26.3	883	2	AAQ15369	Osmotin-1	
C 7	419.8	26.3	884	2	AAQ15370	Encodes C	
C 8	417.8	26.1	741	2	AAV68541	Nucleosid	
C 9	355	22.2	1004	2	AAQ21414	Encodes o	
C 10	189	11.8	906	3	AAQ47993	Arabidops	
C 11	187.4	11.7	902	3	AAQ47227	Arabidops	
C 12	186.8	11.7	735	6	AB214313	Arabidops	
C 13	186.8	11.7	735	7	AB242096	Arabidops	
C 14	186.8	11.7	735	7	AD468525	Arabidops	
C 15	186.8	11.7	950	6	ABN98366	Arabidops	
C 16	168.8	10.6	875	5	ACR84839	Sunflower	
C 17	157	9.8	771	15	AAQ229511	Asparagus	
C 18	144.8	9.1	900	1	AAV90842	Fragment	
C 19	144.8	9.1	900	2	AAV62808	Tobacco P	
C 20	144.8	9.1	900	2	AAV72392	PR-3 majo	
C 21	138.6	8.7	910	4	AAQ04241	Sunflower	
C 22	133.2	8.3	549	3	AAQ55150	Arabidops	
C 23	126.4	7.9	2000	7	ADA71704	Rice gene	

ALIGNMENTS

RESULT 1

ABK90561	ABK90561 standard; DNA; 1598 BP.
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ID	ABK90561 standard; DNA; 1598 BP.
XX	
AC	ABK90561;
XX	
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Potato proteinase inhibitor 1 (pin1)
XX	
KW	Potato; proteinase inhibitor 1; pin1
KW	Controlled Environmental Agriculture
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XX	
OS	Solanum tuberosum.
XX	
PN	WO200259333-A2.
XX	
PD	01-AUG-2002.
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PF	18-JAN-2002; 2002WO-US001287.
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PR	23-JAN-2001; 2001US-0263224P.
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Aa40422	Potato
Aa49091	Diospyros
Aa496184	PR-R major
Aa491491	Zeamatin
Aa428688	Ripening
Aa40215	Gene enco
Aa491063	Rice gene
Aa471064	Rice gene
Aa495396	Arabidops
Aa478707	Nucleotid
Aa459196	Modified
Aa491934	DNA sequ
Aa496303	Rice gene
Aa404913	pinG132CV
Aa404914	pinG132CV
Aa470933	DNA sequ
Aa478703	Nucleotid
Aa450328	Thaumatin
Aa450328	Sequence
Aa406311	Thaumatin
Aa406311	Thaumatin

CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform

SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;

Query Match	99.9%	Score 1596.4;	DB 6;	Length 1598;
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Db	61	AAAAATTGGAAGAAGCGTAGGACCAATGAGCACTGGGTCGCAACAATATGTTGTCCTC	120	
Qy	121	CAAAATGTTGACAGGATGTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTCAC	180	
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Db	241	CGAAAGTCATCGGTATATTAATCCATCACTAAGAAATGTCGCAACAATCTAAGTTGT	300	
Qy	301	TGAATCTGTCGAAGCGTACTCGGCTAGGCTGTTTGGTGGTTCGCCCAACCCCGTGCAC	360	
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Db	661	AATTAATTTTGGTACTTTATATAGGATATGCGGCTTTTGGCAGTACGGATATTAAT	720	
Qy	721	CGTATTAATAACAATATCATCTTTGACATAATTAAGCAATATATTAACAATATGAT	780	
Db	721	CGTATTAATAACAATATCATCTTTGACATAATTAAGCAATATATTAACAATATGAT	780	
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RESULT 2
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 ID ABK90560 standard; DNA; 1595 BP.
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 AC ABK90560;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform I.
 XX
 KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
 KW Controlled Environmental Agriculture; crop cultivation.
 XX
 OS Solanum tuberosum.
 XX
 PN WO200259333-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-JAN-2002; 2002WO-US001287.
 XX
 PR 23-JAN-2001; 2001US-0263224P.
 XX
 PA (DAIZ/) DAI Z.
 PA (SHIL/) SHI L.
 PA (HOOK/) HOOKER B S.
 XX

PI Dai Z, Shi L, Hooker BS;
 XX WPI; 2002-608457/65.
 XX
 PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
 PT isoforms derived from potato, useful in manipulating expression of genes
 PT and in Controlled Environmental Agriculture for heterologous protein
 PT production.
 XX
 XX Claim 2; Fig 1; 43pp; English.
 XX
 CC The invention relates to polynucleotides having proteinase inhibitor 1
 CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
 CC and amt gene promoters are useful in manipulating expression of genes,
 CC particularly in transformed plant cells. The gene promoters are useful in
 CC constructing gene expression vectors and in controlled environmental
 CC agriculture for heterologous protein production. The vectors are useful
 CC in facilitating the expression and/or secretion of heterologous proteins
 CC in cell culture or by crop cultivation. The new gene promoter isoforms
 CC provide high level, stable and controllable expression that is
 CC temporally, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform
 XX
 SQ Sequence 1595 BP; 510 A; 291 C; 297 G; 497 T; 0 U; 0 Other;
 Query Match 92.7%; Score 1480.6; DB 6; Length 1595;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1545; Conservative 0; Mismatches 49; Indels 5; Gaps 3;
 QY 1 GTAATACGACTCACTATAGGCGACCGGTGGTCGACGGCCGGCTGGTATCTTTGTTGA 60
 DB 1 GTAATACGACTCACTATAGGCGACCGGTGGTCGACGGCCGGCTGGTATCTTTGTTGA 60
 QY 61 AAAAATTCGAAAGAACGTAGGACCAACATGACCTGGGTGCAACATATTTGTTGCTC 120
 DB 61 AAAAATTCGAAAGAACGTAGGACCAACATGACCTGGGTGCAACATATTTGTTGCTC 120
 QY 121 CAATGTGGTCAACAGGATGTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTCAC 180
 DB 121 CAATGTGGTCAACAGGATGTTACATCTCCGGGTACTTTAAGCTGACCAGGCAATTCAC 180
 QY 181 CATTTATTTGCGGTGCAATGAATTTGTTGGCAATTTCCCTCCACTGGATTAGTCGGG 240
 DB 181 CATTTATTTGCGGTGCAATGAATTTGTTGGCAATTTCCCTCCACTGGATTAGTCGGG 240
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 DB 541 TGGACAGTTGTTG--CGTACTCGATAGTGGACATAGTGAAGTCAACAAAGCCAGA 598
 QY 601 AGGAGAAACCAAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAATTTATATGTGACA 660
 DB 599 AGGAGAAACCAAAAGAGATCTCAAGTAGGCCCATGTTGTTGAAATTTATATGTGACA 658

QY 661 AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAAT 720
 DB 659 AATTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTACGATATTAAT 718
 QY 721 CGTATATATAACAATATCATCTTTGACTAATATATAAGAAATATATACATATGAT 780
 DB 719 CGTATATATAGCAATATCATCTTTGACTAATATATAAGAAATATATACATATGAT 778
 QY 781 TTGGTAAACGTTGAGGTGGAAAAATGTATAAGAGCGCCCTAATAATATTTTATGA 840
 DB 779 TTGGTAAACGTTGAGGTGGAAAAATGTATAAGAGCGCCCTAATAATATTTTATGA 838
 QY 841 ATATAGCCTATAGTTTCAAGTTAACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 900
 DB 839 ATATAGCCTATAGTTTCAAGTTAACTTTATTTGGTGATTAACCTTTGACATATAAATCTGT 898
 QY 901 AAGCTGACGGAATTTTCTTTAAACCTAAATATATAAAGCAGCTATTTTACATATTTTCG 960
 DB 899 AAGCTGACGGAATTTTCTTTAAACCTAAATATATAAAGCAGCTATTTTACATATTTTCG 958
 QY 961 TGCCAAAGTCTCTTGCACTATCTATCTATGCCCATTCTTTTATCGTTCTAGCCTTC 1020
 DB 959 TGCCAAAGTCTCTTGCACTATCTATCTATGCCCATTCTTTTATCGTTCTAGCCTTC 1018
 QY 1021 TAGGTACAGTTTGAACATAAAATCATAAATTTGAAGTAAATTTAGTTTATTTT 1080
 DB 1019 TAGGTACAGTTTGAACATAAAATCATAAATTTGAAGTAAATTTAGTTTATTTT 1078
 QY 1081 TTCAATATCTCGTATGGATCAATTTGTTAGATCAATCTGAATATATACAAATCTCGAT 1140
 DB 1079 TTCAATATCTCGTATGGATCAATTTGTTAGATCAATCTGAATATATACAAATCTCGAT 1138
 QY 1141 TTTAAATACACACCAATCTCGCTATAGTGGGAAGTCTATGTGATTCGTGGCAAGT-GTTT 1199
 DB 1139 TTTAAATACACACCAATCTCGCTATAGTGGGAAGTCTATGTGATTCGTGGCAAGT 1196
 QY 1200 GATTATTTCTAGTCTAGTTCAGTCAACATTTTATAGTCAATATCTATTAAGAAACC 1259
 DB 1197 GATTATTTCTAGTCTAGTTCAGTCAACATTTTATAGTCAATATCTATTAAGAAACC 1256
 QY 1260 CCTATTTGATGCAAAATATCTATTAAGAAACCCTATTCATCTTATTTTATTTACGAT 1319
 DB 1257 CCTATTTGATGCAAAATATCTATTAAGAAACCCTATTCATCTTATTTTATTTACGAT 1316
 QY 1320 CGGAGCATCGATATTTTACTAATTAATAAATTTGGGAGGAATGATCGACAGCCATC 1379
 DB 1317 CGGAGCATCGATATTTTACTAATTAATAAATTTGGGAGGAATGATCGACAGGTCATC 1376
 QY 1380 AAGCTTATCGTCCGATCCACATAGGATAACGTTAGTATGCGCTGTTTATAGAGAAACAAGT 1439
 DB 1377 AAGCTTATCGTCCGATCCACATAGGATAACGTTAGTATGCGCTGTTTATAGAGAAACAAGT 1436
 QY 1440 GGNATCATGATCAATGAGTTTAAATAATCTCTATTAATAATCTGCTATCCCTCTTAA 1499
 DB 1437 GGNATCATGATCAATGAGTTTAAATAATCTCTCTAATAATCTATATATATCTCTTAA 1496
 QY 1500 CCAATATCATCTAAACACACAAATATAAACTTAGATTCTTAAAGAAATTCAGAAATTA 1559
 DB 1497 CTAAATGATCTAAACACCAATATAAATAGATTCTTTAAAGAAATTCAGAAATTA 1556
 QY 1560 ATGGAGGCAAAATAGTCTATGTTGAGTTGTTGTTTC 1598
 DB 1557 ATGGAGGCAAAATAGTCTATGTTGAGTTGTTGTTTC 1595
 RESULT 3
 ABK90562
 ID ABK90562 standard; DNA; 1546 BP.
 XX AC ABK90562;
 XX XX
 DT 15-NOV-2002 (first entry)
 XX XX

Potato proteinase inhibitor 1 (pin1) gene promoter isoform III.

Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
Controlled Environmental Agriculture; crop cultivation.

Solanum tuberosum.

WO200259333-A2.

01-AUG-2002.

18-JAN-2002; 2002WO-US001287.

23-JAN-2001; 2001US-0263224P.

(DAIZ/) DAI Z.

(SHIL/) SHI L.

(HOOKER) HOOKER B S.

Dai Z, Shi L, Hooker BS;

WPI; 2002-608457/65.

New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter isoforms derived from potato, useful in manipulating expression of genes and in Controlled Environmental Agriculture for heterologous protein production.

Claim 2; Fig 3; 43pp; English.

The invention relates to polynucleotides having proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1 and amt gene promoters are useful in manipulating expression of genes, particularly in transformed plant cells. The gene promoters are useful in constructing gene expression vectors and in Controlled Environmental Agriculture for heterologous protein production. The vectors are useful in facilitating the expression and/or secretion of heterologous proteins in cell culture or by crop cultivation. The new gene promoter isoforms provide high level, stable and controllable expression that is temporarily, environmentally, or developmentally regulatable. This sequence represents a potato pin1 gene promoter isoform

Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match 84.1%; Score 1344; DB 6; Length 1546;

Best Local Similarity 94.1%; Pred. No. 5.7e-291;

Matches 1462; Conservative 0; Mismatches 81; Indels 10; Gaps 6;

49 ATCTTTGTTGAAAAAATTGGAAAAGAACGTTAGGACCAACATGACCTTGGGTGCAACAAT 108

1 ATCTTTGTTGAAAAAATTGGAAAAGAACGTTAGGACCAACATGACCTTGGGTGCAACAAT 60

109 ATTGTTGCTCCCAAAATGTGTGACAAAGATTGTACATCTCCGGGTACTTTAAGCTGAC 168

61 ATTGTTGCTCCCAAAATGTGTGACAAAGATTGTACATCTCCGGGTACTTTAAGCTGAC 120

169 TAGGACATTACCACTTTATATTTCCTCGGTGCAATTTGTTGGCAATTTCCCTCCCACTTG 228

121 TAGGACATTACCACTTTATATTTCCTCGGTGCAATTTGTTGGCAATTTCCCTCCCACTTG 180

229 GATTAGTGGGGGGAAGTCACTCGGTATATTAATCCATCACTAAAGAAATGTCACAGA 288

181 GATTAGTGGGGGGAAGTCACTCGGTATATTAATCCATCACTAAAGAAATGTCACAGA 240

289 AATCTAGTTGTTGCACTGTTCCCAAGCGTACTCGGTAGGTGTTTGGTGGTGGTGGCCCC 348

241 AATCTAGTTGTTGCACTGTTCCCAAGCGTACTCGGTAGGTGTTTGGTGGTGGTGGCCCC 300

349 ACCCGGTGCACTGAGGACCAACCAATCACTCGGTATGTCAGCAAGACCTCTACAGCAC 408

301 ACCCGGTGCACTGAGGACCAACCAATCACTCGGTATGTCAGCAAGACCTCTACAGCAC 360

409 CACCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAGGCGCAT 468

361	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTTAGGCGCAT	420
469	CAATGACCCACATTTGGCTCGATCGAGACGTCGGGACCGCCCTATC-GGGTCGATGCGG	527
421	CAATGACCCACGTTTGGCTCGATCGAGACGTCGGGACCGCCCTATCGGGGTCCATGCTG	480
528	CCCAAAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGAAGTGAAGT	587
481	CCGACGCGTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAGTGAAGT	538
598	CACAAAACGCGAGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTGTTGAAAT	647
539	CACAAAACGCGAGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTGTTGAAAT	598
648	TTATATGTGGCAAAATATTTTGGTACTTTATATATAGGGATAGGGCGCTTTGGCAC	707
599	TTATATGTGGCAAAATATTTTGGTACTTTATATATAGGGATAGGGCGCTTTGGCAC	658
708	TACGATATTAATCGTATATATTAACATATCATCTTTGACTAATTTATAAAGCAATAT	767
659	TATGATATTAATCGTATATTAATTAACATATCATCTTTGACTAATTTATAAAGCAATAT	718
768	ATTACAAATATGATTTGGTAAACGTTGAGTGGAAAAATGTATAAGAGCCGCTTAATTT	827
719	ATTACAAATATGATTTGGTAAACGTTGAGTGGAAAAATGTATAAGAGCCGCTTAATTT	778
828	AATATTTTATGATATAGCCCTATAGTTACAGTTAACTTTATTTGGTGATACCTTGAC	887
779	AATATTTTATGATATAGCCCTATAGTTACAGTTAACTTTATTTGGTGATACCTTGAC	838
888	ATATAAACCTGTGAACGTCGAGCAATTTTCTTAAACCTAAATATTTAAAGCAGCTATT	947
839	ATATAAACCTGTGTATGTCGAGCAATTTTCTTAAACCTAAATATTTAAAGCAGCTATT	898
948	TTCACTATTTTGGTGGCAAAAGTCTCTTGCAATATCTATGTCCTATTTTACTTTTAT	1007
899	TTAATATTTTGGTGGCAAAAGTCTCTTGCAATATCTATGTCCTATTTTACTTTTAT	958
1008	CGTCTGACCTCTAGGTACAGTTGGAACATATAAATCATATAAATTTGAAAGTAAAAA	1067
959	CGTCTGACCTCTAGGTACAGTTGGAACATATAAATCATATAAATTTGAAAGTAAAAA	1018
1068	TTAGTTTCTTTTCTATTAATCTAGTATGATCAATTTGTTAGATCAATCTGAAATATAC	1127
1019	TTAG---TTTCTTTCTATTAATCTAGTATGATCAATTTGTTAGATCAATCTGAAATATAC	1075
1128	AAACCATTTCTGATTTTAAATCACAACCATTTCTGCTTAATGGGAGTCTAT-GTGATTC	1186
1076	AAATCATTTCTGATTTTAAATCATAACTATTTCTGATGAGGAAACGCTCTATGTTGATTC	1135
1187	GTGGCAAGTGTGTA-TTATTTCTAGTCTAGATGGAGTCAAACTTTTGTAGTCAAAATAT	1245
1136	GTGACAGTGTGTTGATTTATTTCTAGTCTGATGGAGTCAAACTTTTGTAGTCAAAATAT	1195
1246	CTATTAAAGAACCCCTATTTGATGCAATATCTATTTAAAGAACCCCTATTTCACTTTA	1305
1196	CTATTAAAGAACCCCTATTTGATGCAAAAGTCAATAAA--TATTTAATATCATCTTTA	1253
1306	TTTATTTTACGATCGGAGCATGGATATTTTACTAATTTAAATTTAAATTTGGAGGAATTG	1365
1254	TTTATTTTACGATCGGAGCATGGATATTTTACTAATTTAAATTTAAATTTGGAGGAATTG	1313
1366	ATCGAACGCAATCAAGCTTATCGTTCGATCCCATTTAGGATAAGCTTAGTATGCTGTTT	1425
1314	ATCGAACGCAATCAAGCTTATCGTTCGATCCCATTTAGGATAAGCTTAGTATGCTGTTT	1373
1426	TTAGGAACCAAGTGGATCATGTAATTTGAGTTGTTAAATATATCTCTTATAAATACCTGT	1485
1374	TTAGGAACCAAGTGGATCATGTAATTTGAGTTGTTAAATATATCTCTTATAAATATCTAT	1433
1486	CTATCCCTCTTAAACCAAAATACATCTAACACACAAAATATATAAATTTAGATTCCTTAAAGA	1545

Db 1434 ATATACCTCTAAACTAAATGCATCTAACAACAACAATAAATTAAGTCTTTAAAGA 1493
 QY 1546 AATTCAGAAATTAATGGAGCAATAAGTCTATGCTGAAGTTGTTCTTTC 1598
 Db 1494 AATTCAGAAATTAATGGAGCAATAAGTCTATGCTGAAGTTGTTCTTTC 1546

RESULT 4

AAV52754/c
 ID AAV52754 standard; DNA; 3033 BP.

XX AC AAV52754;

XX DT 02-NOV-1998 (first entry)

XX DE Nicotiana tabacum osmotin gene with promoter.

XX KW Nicotiana tabacum; tobacco plant; osmotin gene; promoter; inhibition;
 XX KW fungal pathogen; insect pathogen; nematode pathogen; viral pathogen; ds.
 XX OS Nicotiana tabacum.

XX FH Key Location/Qualifiers
 XX FT CDS 2034..2774
 XX FT /*tag= a
 XX FT /product= "osmotin"
 XX FT /transl_except= (pos:2574..2576,aa:Arg)

XX PN US5801028-A.

XX XX 01-SEP-1998.

XX PD 07-JUN-1995; 95US-00482037.

XX PF 20-MAY-1993; 93US-00065147.

XX PR 12-JAN-1994; 94US-00180428.

XX XX (PURD) PURDUE RES FOUND.

XX PI Hasegawa PM.; Bressan R;

XX DR WPI; 1998-494773/42.

XX DR P-PSDB; AAW69751.

XX PT Inhibition of pathogens in plants by recombinant expression of pathogen
 XX PT inhibiting proteins - uses nucleic acid constructs containing the
 XX PT pathogen inhibiting proteins under control of osmotin promoter, which is
 XX PT inducible by specific signals.

XX PS Claim 1; Col 29-34; 26pp; English.

XX CC A method has been developed of inhibiting a pathogen in a plant. The
 XX CC method comprises: (a) providing or constructing a vector comprising an
 XX CC osmotin promoter and foreign DNA sequence encoding a pathogen-inhibiting
 XX CC protein, where the promoter is operably linked to the foreign DNA
 XX CC sequence and includes: (i) nucleotide sequence 5' of the osmotin coding
 XX CC sequence extending to position -248 bases from the start of the osmotin
 XX CC protein coding sequence, the coding sequence defined as starting at bp
 XX CC 2034 of the 3033 bp osmotin sequence (present sequence), (ii) a
 XX CC nucleotide sequence which hybridizes to (i) and promotes expression of an
 XX CC operably linked coding sequence under conditions of desiccation; and (b)
 XX CC introducing the vector into the plant to create a transformed plant,
 XX CC where expression of the pathogen-inhibiting protein in the transformed
 XX CC plant is regulated by the osmotin promoter. The method is useful for the
 XX CC production of recombinant plants having genes under control of an osmotin
 XX CC promoter, especially of pathogen inhibiting proteins. Osmotins are
 XX CC cationic plant proteins, similar to tobacco PR-5-type proteins. The
 XX CC osmotin genes are under control of hormonal or environmental signals,
 XX CC including abscisic acid, ethylene, tobacco mosaic virus invention,
 XX CC salinity, desiccation and wounding. The present sequence represents the
 XX CC Nicotiana tabacum osmotin gene with promoter

XX SQ Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;

Query Match 29.3%; Score 468.8; DB 2; Length 3033;
 Best Local Similarity 76.8%; Pred. No. 5.6e-95;
 Matches 679; Conservative 0; Mismatches 162; Indels 43; Gaps 7;

QY 46 GGTATCTTTGTTGAAAAAATTCGAAAGAACCTAGAGACACATGACCTTGGTGGTCAAC 105
 Db 2622 GGCATCTTTGTTGAAAAAATTTTGAGAAAAATAGGACCAAGGTCCTTGTGTGCAAC 2563
 QY 106 AATATTGTTCTCTCCAAATGCTGTAAGAGATTGTTTACATCTCTCGGGTACTTTAAGCT 165
 Db 2562 AATATTGTTCTCTCGAATGTAAGAGATTGTTTACATCTCTCGGGAACCTAAGTT 2503
 QY 166 GACTAGGACATTCACCATTTATATTTCGGTGCATTAATTTGTTGTCATTTCCCTCCAC 225
 Db 2502 CGCGGGGACATTCGCGGTTTATATTAGCCGTACAAATGAATTCATGGCATTTCCCTCCAC 2443
 QY 226 TTGGATTAGTCGGGGCGAAGTTCATCGGTATATTAATCCATCAACTAAGAAATCTCC 285
 Db 2442 TAGGTTAGTCGGGGCGAAGTTCATCGGAATGTTGAATCCATCAACTAAGAAATCTCC 2383
 QY 286 AGAAATCTAAGTTGTTGAATGCTGCTCAAGGCGTACTCGGCTAGGGTGTGTTGGTGTTC 345
 Db 2382 AGAAATCTAAACCACTGAATTTGCTCCAAAGCGTATTCAGCAAGGTTTGGTGGTTAC 2323
 QY 346 CCCACCGGTCGACTCGAGGACACACACCAATCACAGTATGACGAGAACCTCTACCAG 405
 Db 2322 CCCACCGGTCGACTGTAGGACTCCACCAAGTCCACCGGTTTGGCACGTACCCCTACCAG 2263
 QY 406 CACCACGAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGCGG 465
 Db 2262 CAGCAATTGAATTACAATTAGTAGGCGCCCATACACATGTCCTTTAGTACCTCTGGGCG 2203
 QY 466 CATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGACCGCCTATCGG-GTCCATG 524
 Db 2202 CATTGATCACCCAAAGTTTGGCTCGATCGAGACCGCGGCGACCGCTATGGGTGTGCGAG 2143
 QY 525 CGGCCCAAGCATGTATGACACGTTCTGCGCGTACTCTCGATAGTCACAGCATAAGTGA 584
 Db 2142 CCGCCCAAGCGGTGTACGACAGTTGTT--TCGGACCTCGATAGTGGCAGCATTAAGTATA 2085
 QY 585 AGTCACAAAAGCCAGAGGAGAAACCAAAAGAAGATCTCAAGTAGCCCATGTTGTTTGA 644
 Db 2084 AGTCACCAAGGCAAGGAGGAAGAAACAAAGAAGATCTCAAGTTGCCCATGTTGTTGA 2025
 QY 645 AATTATATGTGACAAATTAATTTTGGTACT-----TTATATATA 685
 Db 2024 CATTTTAAACAGTTGGTGTGATATAGTGACAAATTTGTTAGTGGTTTATATA 1965
 QY 686 GGGATATGGCGGCTTTTGGCAGCTACCGATATTAAATCGTATTATATAACAATATCATCTT 745
 Db 1964 GGGGAATGGCGCTTTTCGTACTATGATATTAATC-----ATAATATTATTATACATT 1910
 QY 746 TGACTAATTATAAAGCAATATATATTAACAATATGATTTGGTAAACGTTGAGTGG-AAAAA 804
 Db 1909 TGACTA---ATAAAGGATATATCTCAAGGATGCTTTGGCAAGATGAGAGGCGGCTTA 1853
 QY 805 TGTATAGAGCGCGCTTAATAATTAATTTTATGAATATAGCTATAGTTACACAGTTAA 864
 Db 1852 ACATTAAGAGCGCGCTTAATTAATTTTATGAATATAG-----AAGTCA 1805
 QY 865 CTTTATTTGGTGAATCTTTGACATATAAATCTCTGTACGTGAC 908
 Db 1804 ATTTATTTGGTAATACCGTGCACCTATAATCTCTGTACGTGAC 1761

RESULT 5

AAK16340/c

ID AAK16340 standard; DNA; 3033 BP.

XX AC AAK16340;

XX DT 26-APR-1999 (first entry)

Encodes C-terminally truncated osmotin-like antifungal protein.

tobacco: osmotic tolerance: AP20: ss.

Nicotiana tabacum.

QY 525 CCGCCAAACGATGATGACAGTGTGTTGGCGGTACCTCGATAGTGACAGCATAAGTGAA 584
 DB 125 CCGCCAAACGTTGTACGACAGTGTGTT--TCGGACCTCGATAGTGACAGCATAAGTATA 68
 QY 585 AGTCACAAAGCCGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
 DB 67 AGTCACAAAGCCGAGAGGAGAAACCAAAAGAGATCTCAAGTTGCCCATGT 15
 RESULT 8
 ID AAV68641/c
 AC AAV68641 standard; DNA; 741 BP.
 XX
 XX AAV68641;
 DT 12-MAR-1999 (first entry)
 DE Nucleotide sequence of the osmotin AP24.
 XX
 XX Osmotin AP24; beta-(1,6)-glucanase; bG; chimeric DNA;
 KW anti-fungal composition; transgenic plant; pathogen resistant; ds.
 XX
 XX Nicotiana tabacum.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..741
 FT /*tag= a
 FT /product= "osmotin AP24"
 XX
 PN WO9849331-A1.
 XX
 XX 05-NOV-1998.
 PD
 XX 27-APR-1998; 98WO-EP002580.
 PF
 XX 29-APR-1997; 97EP-00201254.
 PR
 XX (MOGE-) MOGEN INT NV.
 PA
 XX
 PI Stuiver MH, Lageweg W, Van Deventer- Troost JPE, Custers JHHV;
 XX
 DR WPI; 1999-024066/02.
 DR P-PSDB; AAW80986.
 XX
 PT Isolated protein with beta-glucanase activity - is isolated from edible
 PT fungus and used to produce pathogen resistant plants.
 XX
 PS Claim 13; Page 27-28; 47pp; English.
 XX
 CC This is the nucleotide sequence encoding the Nicotiana tabacum osmotin
 CC AP24, used in the method of the invention in conjunction with beta-(1,6)-
 CC glucanase (bG) to produce a chimeric DNA. Osmotin AP24 and beta-(1,6)-
 CC glucanase (bG) can be used in an anti-fungal composition. The chimeric
 CC DNA sequences can be transferred into plants to make them pathogen
 CC resistant
 XX
 SQ Sequence 741 BP; 182 A; 173 C; 178 G; 208 T; 0 U; 0 Other;
 Query Match 26.1%; Score 417.8; DB 2; Length 741;
 Best Local Similarity 83.9%; Pred. No. 1e-83; Gaps 2;
 Matches 496; Conservative 0; Mismatches 92; Indels 3; Gaps 2;
 QY 46 GGTATCTTTGTTGAAAGAAATGGAAGAACGTAGGACACACATGGACCTTGGGTGCAAC 105
 DB 589 GGCATCTTTGTTGAAAGAAATTTGAGAAATATGAGCACCACAGGTCTTGTGTGCAAC 530
 QY 106 AATATTGTTGCTCCAAATGTTGTACAGAGATTGTACATCTCCCGGTACTTTAAGCT 165
 DB 529 AATATTGTTGCTCCGAAATGTATACAGAGTTTATTACATCTCCCGGAACCTTAAGTT 470
 QY 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATTGAATTGTGTGGCATTTCCCTCCAC 225

DB 469 CCGCGGGAATTCGCCGTTTATTATTAGCCGTACAAATGAATTCATGGCATTTCCCTCCAC 410
 QY 226 TTGGATTAGTCGGGCGGAAAGATCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
 DB 409 TAGGGTTAGTCGGGCGGAAAGATCATCGGAATGTTGAATCCATCAACTAAAGAAATGTCCC 350
 QY 286 AGAAATCTAAAGTTGTTGAACTGGTCCAAAGGCGTACTCGGCTAGGGTGTGTTGGTGGTTGC 345
 DB 349 AGAAATCTAAACCACTGAATTGGTCCAAAGCGTATTTCAGCCCAAGGTGTTGGTGGTTTAC 290
 QY 346 CCCACCCGTCGACTGCAGGACACCAATCACCAGTATGCACGAACCTCTTACCAG 405
 DB 289 CCCACCCGTCGACTGTAGGACTCCACCACAGTACCGGTTTGGCAGCTACCCCTACCAG 230
 QY 406 CACCACCGAAGTTACATCCAGTACGACCCCAATACATGTCGTCATCGTGGTCCCTTAGGCG 465
 DB 229 CAGCATTTGAAGTTACAAATTAGTACGGCCCAATACACGTGCCATTTTAGTACCTCGTGGCG 170
 QY 466 CATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGCGACCGCTATCGG-GTCCGATG 524
 DB 169 CATTGATCACCAGTTTGGCTCGATCGAGACGCGCGCCCTATGGTGGTGTGACG 110
 QY 525 CCGCCCAACGATGTATGACAGATTGTTGGCGGTACCTCGATAGTGACAGCATAAAGTAA 584
 DB 109 CCGCCCAACGCGTGTACGACAGTTGTT-TCGGACCTCGATAGTGGCAGCATAAAGTATA 52
 QY 585 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCAT 635
 DB 51 AGTCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTTGCCCAT 1
 RESULT 9
 ID AAQ21414/c
 AC AAQ21414 standard; DNA; 1004 BP.
 XX
 XX AAQ21414;
 DT 10-JUN-1992 (first entry)
 DE Encodes osmotin-like protein from tobacco plant.
 XX
 KW drought tolerance; salt tolerance; environmental stress; ss.
 XX Nicotiana tabacum.
 FH Key Location/Qualifiers
 FT sig_peptide 18..80
 FT /*tag= a
 FT mat_peptide 81..773
 FT /*tag= b
 FT /product= "osmotin_like_protein"
 XX
 PN JP04018099-A.
 PD 22-JAN-1992.
 XX
 XX 10-MAY-1990; 90JP-00121816.
 XX 10-MAY-1990; 90JP-00121816.
 XX (NAGS) NAGASE SANGYO KK.
 PA
 XX WPI; 1992-075255/10.
 DR P-PSDB; AAR21426.
 XX
 PT Amino-acid sequence for protein resembling osmotic - for prodn. of higher
 PT plants resistant to stress such as drought, salt etc.
 XX
 PS Claim 3; Fig 1; 10pp; Japanese.
 XX
 CC The protein encoded by this DNA is an osmotin-like protein involved in
 CC resistance to stress in higher plants. Stress may be caused by e.g. viral
 CC infection, drought, high salt concentration, etc. See also AAQ21415-8.

XX	SQ	Sequence 1004 BP; 288 A; 200 C; 211 G; 305 T; 0 U; 0 Other;	XX	25-FEB-1999;	99US-0121825P.
		Query Match 22.2%; Score 355; DB 2; Length 1004;	PR	05-MAR-1999;	99US-0123180P.
		Best Local Similarity 76.5%; Pred. No. 1.2e-69;	PR	09-MAR-1999;	99US-0123548P.
		Matches 461; Conservative 0; Mismatches 140; Indels 2; Gaps 2;	PR	23-MAR-1999;	99US-0125788P.
			PR	25-MAR-1999;	99US-0126264P.
QY	49	ATCTTTGTTGAAAAATTTGGAAGACGTAGGACCACTGGACCTTGGTGCAACAAT 108	PR	29-MAR-1999;	99US-0126785P.
Db	606	ATCTTTGTTGAAACCATTTGTAATCTAGTAGGACCACTGGTGCAACAAT 547	PR	01-APR-1999;	99US-0127462P.
QY	109	ATTTGTTGCTTCAAAATTTGGTACAGGATGTTTACATCTCTCGGGTACTTTAAGCTGAC 168	PR	06-APR-1999;	99US-0128234P.
Db	546	ATTTGTTGCTTCAAAATTTGGTACATGGTGTGTTACATCTCTCCAGTACCTAAGTGAAC 487	PR	08-APR-1999;	99US-0128714P.
QY	169	TAGGACATTCACATTTATTTGCGTGGCATTTGTTGGCATTTCCCTCCACTTG 228	PR	16-APR-1999;	99US-0129845P.
Db	486	CAGGCAATTCACATTTATTTGCGTGGCATTTGAAATTCGTTGATTTTCCAGGACCAAG 427	PR	19-APR-1999;	99US-0130077P.
QY	229	GATTAGTCGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGCCCCAGA 288	PR	21-APR-1999;	99US-0130449P.
Db	426	GCTTAGTCGGGCGAAAGACATAGGAATGTTAAATCCATCAATACAGAGATGCCCCAGA 367	PR	23-APR-1999;	99US-0130510P.
QY	289	ATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGCTAGGGTGTGTTGGTGGTTGCCCC 348	PR	28-APR-1999;	99US-0130891P.
Db	366	AATCTAAGTTGCTGAATTTGTTTCAACGGGTATTCGGCTAAGGTATTTGGTGGTTTACCCC 307	PR	30-APR-1999;	99US-0131449P.
QY	349	ACCCGGTGCACTGCAGGACACACCAATCACCAGTCATGCAGAACTCTACACGAC 408	PR	04-MAY-1999;	99US-0132048P.
Db	306	ATCTTTGCACTTCTAAGACTTCACCAATCACCAGTTTGGACCAACTCTACAGGAC 247	PR	06-MAY-1999;	99US-0132484P.
QY	409	CACGAACTTACATCAGTAGACACCCCATATACGTGCCATCGTAGTGCCTCCCTAGGCGCAT 468	PR	06-MAY-1999;	99US-0132486P.
Db	246	CATCAAGTTGCAATTTAGTAGACACCCCATATACGTGCCATTTTGTGTCAGGTTGCGCC 187	PR	06-MAY-1999;	99US-0132487P.
QY	469	CAATGACCCACATTTGGCTGATCGACGCTCGGCGACCCGCTA-TCGGGTCGATCGC 527	PR	07-MAY-1999;	99US-0132863P.
Db	186	AGAACCCACATTTGACCTGTTTGGAGACGTGCGCCACGGCTACAGGGGTTCGCGCTG 127	PR	11-MAY-1999;	99US-0134256P.
QY	528	CCCAACAGTGTATGGACAGTTGTTT-GCGGTACCTCGATAGTGACACATAGTGAAG 586	PR	14-MAY-1999;	99US-0134219P.
Db	126	CCCAACGGTGTATGGGCAATTTGTTATGGACTTCAANTACCGCGGAACATAAGTAAAG 67	PR	14-MAY-1999;	99US-0134218P.
QY	587	TCACAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAA 646	PR	14-MAY-1999;	99US-0134218P.
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QY	647	TTT 649	PR	18-MAY-1999;	99US-0136392P.
Db		6 TTT 4	PR	20-MAY-1999;	99US-0136782P.
			PR	01-JUN-1999;	99US-0137222P.
RESULT 10			PR	04-JUN-1999;	99US-0137528P.
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XX			PR	14-JUN-1999;	99US-0139119P.
DT 18-OCT-2000 (first entry)			PR	16-JUN-1999;	99US-0139452P.
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KW Hybridisation assay; genetic mapping; gene expression control;			PR	18-JUN-1999;	99US-0139459P.
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KW promoter; termination sequence; ss.			PR	18-JUN-1999;	99US-0139461P.
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PR	13-AUG-1999;	99US-0148565P.			
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<p>Query Match 11.8%; Score 189; DB 3; Length 906; Best Local Similarity 61.7%; Pred. No. 1.8e-32; Matches 377; Conservative 0; Mismatches 215; Indels 19; Gaps 4;</p>					
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Db	619	GGCATCTCTGCTTAAAGAACTCTTGAGTAGTCAGTAGCTACATGATCCCTGACCGTTTCG	560		
QY	100	TGCAACAATATTTGTCCTCCAAATGTTGGTACAAAGATTGTTACATCTCCGGGTACTT	159		
Db	559	TACAAACAGTATTTGGTTCGTCGTAATACAGTACACGGGTGTTGTCATCCACCTGGGGCTC	500		
QY	160	TAAAGCTGACTAGGACATTCACCATTTATATTTGCGTGCATTTGAATTTGTTGGCATTTCC	219		
Db	499	TCACACGTTTGGACATTTGTCGTTTATGTTGTTGTTACATAGTATCCGATGGCGATTC-	441		
QY	220	CTCCACTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAATTAATCCATCACTAAAGAAA	279		
Db	440	-----GAACTAGTTGGGCTTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA	389		
QY	280	TGTCCTCCAGAAATCTAAGTTTGTGAACCTGGTCCAAAGGCTACTCGGCTAGGGTGTGGTG	339		
Db	388	TATCGTAGAAGTCTAAGTTTGTGAATTTGTTTCAAGGCTACTCAGCCACGTTGTTGGTG	329		
QY	340	GTTTGGCCCCCCTGGTGCATCTGCAGGACACCAACCAATACCAAGTATGACCAAACTC	399		
Db	328	GGTGTCCCGCAGCAGTACATTTGGAGTCCACCACTGCAGTCACCAAGTTTGGCATCGGCCAC	269		
QY	400	TACGAGCACCACCGAAGTTACATCCAGTACGACCCCATATACGTAGGCTATGTCGCC	459		
Db	268	GACCTGAGGAGTCAAAGTTACAATTTGGTCTTACCCCAATCCGTGCAATTTAGTGCCCG	209		
QY	460	TAGGGCGCATCAATGACCCACCATTTGGCCTCGATCGAGACGTCGGGGCACCGCTATCGGGT	519		
Db	208	CCGCGACATCTAGCCTCCATGATTGGCCAGCATCTTAGAGCTCGGCCACCTCC--AGGGCT	151		
QY	520	CGATCCCGCCCAACGATGTATGACAGTTGTTGGCGGTACTCTGATAGTGACAGCATAA	579		

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Db      150 TCGGCAGCCACACGGGTGAACATGTT--TAGGATTGCAATGCGGCGCTTT 93
Qy      580 GTGAAGTCACAAAGCCAGAGGAGAAACCAAGAGATCTCAAGTAGCCCAATGTT 639
Db      92  GCGGTGGAGATGAGCAAAAGTGGCGMAATATGAAGTAGAGACCAAGAGGTTTGCCATT 33
Qy      640 GTTGAATTTA 650
Db      32  TTTTAGTTCTA 22

RESULT 11
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XX AAC47227 standard; DNA; 902 BP.
AC AAC47227;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR	12-AUG-1999;	99US-0148319P.	Db	555	TACAACAGTATTGGTTGCTCGTCTGAATAACAGTACACGGGTGTTGTCATCCACTGGGGTC	496
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PR	17-AUG-1999;	99US-0149175P.	Db	436	-----GAACTAGTTGGCTAAACTCCATAGGTATGTTAAATCCATCGACAGTGAGA	385
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PR	22-OCT-1999;	99US-0160980P.	PR	XX		
PR	22-OCT-1999;	99US-0160981P.	PR	XX		
PR	22-OCT-1999;	99US-0160981P.	PR	XX		
PR	25-OCT-1999;	99US-0161404P.	PR	XX		
PR	25-OCT-1999;	99US-0161405P.	PR	XX		
PR	25-OCT-1999;	99US-0161406P.	PR	XX		
PR	26-OCT-1999;	99US-0161359P.	PR	XX		
PR	26-OCT-1999;	99US-0161360P.	PR	XX		
PR	26-OCT-1999;	99US-0161361P.	PR	XX		
PR	28-OCT-1999;	99US-0161920P.	PR	XX		
PR	28-OCT-1999;	99US-0161922P.	PR	XX		
PR	28-OCT-1999;	99US-0161993P.	PR	XX		
PR	29-OCT-1999;	99US-0162142P.	PR	XX		

Query Match 11.7%; Score 187.4; DB 3; Length 902;
 Best Local Similarity 61.5%; Pred. No. 4e-32;
 Matches 376; Conservative 0; Mismatches 216; Indels 19; Gaps 4;

XX WPI; 2002-304127/34.
 XX Identifying a stress condition to which a plant cell has been exposed and
 XX producing plants with increased tolerance to these abiotic stresses.
 XX PS Claim 144; SEQ ID NO 2118; 577pp + Sequence Listing; English.
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 XX Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;
 SQ
 Query Match 11.7%; Score 186.8; DB 6; Length 735;
 Best Local Similarity 62.4%; Pred. No. 5.2e-32;
 Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;
 QY 46 GGTATCTTTGTTGAAAAAATGGAAAGACGTAGGACACATG-----GACCTTGGG 99
 Db |||||
 QY 586 GGCATCTCTGTTAAAGAAATCTTGAGTACTCAGTATCGCTACATGATCCCTGACCGTTGG 527
 Db |||||
 QY 100 TGCACATATTTGTTCTCCCAATGTTGTTACAGGATTTTACATCTCCGCTACTT 159
 Db |||||
 QY 526 TACACAGTATTTGTTCTGTTAAATACAGTACAGGTTTGTTCATCCACTGGGGCTC 467
 Db |||||
 QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGTGCATTGATTTGTTGGCATTTCC 219
 Db |||||
 QY 466 TCAACACGTTTGGACATTTGCGTTTATGTTCTGGGTACATAGTATCCGATGGCAGTTC- 408
 Db |||||
 QY 220 CTCACATTTGATTCGGGGGAAAGTCAGTATTTAAATCCATCACTAAAGAA 279
 Db |||||
 QY 407 -----GAACTAGTTGGGCTAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGA 356
 Db |||||
 QY 280 TGTCCAGAAATCTAAAGTTGTTGAATCTGGTCCAAAGCGCTACTCGGTAGGTGTTGGTG 339
 Db |||||
 QY 355 TATCGTAGAGTCTAAGTTGTTGATTTGTTTCAAGCGTATCTAGCCAACTGTTTGGTG 296
 Db |||||
 QY 340 GTTTCGCCACCCCGGTGCACCTGCAGGACACCAACCAATACCAAGTATGACGAACTC 399
 Db |||||
 QY 295 GCTGTCCCGCAGCAGTACATTTGGAGTCCACCACTGCAGTCCAGTTTGGCATCGGCCAC 236
 Db |||||
 QY 400 TACCAACACCCAGGATTTACATCCAGTACGACCCCATATACGTGCGCATGTAGTGGCC 459
 Db |||||
 QY 235 GACCTGAGAGTCAAGTTTCAATTTGTTTCAAGCGTATCTAGCCAACTGTTTGGTGGCC 176
 Db |||||
 QY 460 TAGCGCATCATCAATGACCCACATTTGGCTCGATCGAGACGTGGGGCCACCGCTATCGGGT 519
 Db |||||
 QY 175 CCGGACATCTAGCTTCCATGTTGGCCAGCATCTAGACGTGGCCACCTCC--AGGGCT 118
 Db |||||
 QY 520 CGATGCCGCCCAAGCATGTATGACAGTTTGTGGCGTACTCTGATAGTACAGCAATA 579
 Db |||||
 QY 117 TSCGGCAGCCACACGGTGTAACTACATTTGTT--TAGGATTTCCAAATGTGGCGGCTGT 60
 Db |||||
 QY 580 GTGAAGTTCACAAAGCCAGAGGAGAAACCAAAAGAAAGATCTCAAG 627
 Db |||||
 QY 59 CGGTGGAGATCAGCAAAAGTGGCGAAATATGAAAGTAGAGACCAAG 12
 Db |||||
 RESULT 13
 ID ABZ42096/c
 XX ABZ42096 standard; cDNA; 735 BP.
 AC ABZ42096;

XX 27-FEB-2003 (first entry)
 XX Arabidopsis thaliana gene #80 modulated by PTGS.
 XX Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
 XX ss.
 XX Arabidopsis thaliana.
 XX Key Location/Qualifiers
 XX CDS 1..735
 XX /*tag= a
 XX WO200281695-A2.
 XX 17-OCT-2002.
 XX 05-APR-2002; 2002WO-EP003806.
 XX 06-APR-2001; 2001US-0282049P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX (FRIE-) FRIEDRICH MIESCHER INST.
 XX Zhu T, Glazov EA, Meins F, Wang X, Chang H;
 XX WPI; 2003-103337/09.
 XX P-PSDB; ABP81252.
 XX Novel polynucleic acid segment useful for modulating gene expression
 PT within a cell by posttranscriptional gene silencing, and for augmenting a
 PT plant cell genome.
 XX Claim 18; Page 324-325; 438pp; English.
 XX The invention relates to a novel isolated polynucleic acid segment
 CC modulated within a cell by posttranscriptional gene silencing (PTGS). The
 CC invention specifically relates to a method to identify an expression
 CC product that is modulated by PTGS. The polynucleotide is useful for
 CC modulating the gene expression within a cell by PTGS, by introducing the
 CC polynucleic acid into a cell and expressing the nucleic acid segment in
 CC the cell to form a product. The polynucleic acid segment is also useful
 CC for augmenting a cell genome, and for augmenting a plant genome, by
 CC contacting a plant cell with the segment to produce a transformed plant
 CC cell, and growing the transformed plant cell to produce a differentiated
 CC transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent
 CC segments of A. thaliana cDNA modulated by PTGS
 XX
 XX Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;
 SQ
 Query Match 11.7%; Score 186.8; DB 7; Length 735;
 Best Local Similarity 62.4%; Pred. No. 5.2e-32;
 Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;
 QY 46 GGTATCTTTGTTGAAAAAATGGAAAGACGTAGGACACATG-----GACCTTGGG 99
 Db |||||
 QY 100 TGCAACATATTTGTTCTCCCAATGTTGTTACAGGATTTTACATCTCCGCTACTT 159
 Db |||||
 QY 526 TACACAGTATTTGTTCTGTTAAATACAGTACAGGTTTGTTCATCCACTGGGGCTC 467
 Db |||||
 QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGTGCATTGATTTGTTGGCATTTCC 219
 Db |||||
 QY 466 TCAACACGTTTGGACATTTGCGTTTATGTTCTGGGTACATAGTATCCGATGGCAGTTC- 408
 Db |||||
 QY 220 CTCACATTTGATTCGGGGGAAAGTCAGTATTTAAATCCATCACTAAAGAA 279
 Db |||||
 QY 407 -----GAACTAGTTGGGCTAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGA 356
 Db |||||
 QY 280 TGTCCAGAAATCTAAAGTTGTTGAATCTGGTCCAAAGCGCTACTCGGTAGGTGTTGGTG 339
 Db |||||

Db 355 TATCGTAGAAGTCTAAGTTGTTGAATTGGTTCAAAGCGTACTAGCCAAAGTGTGTTGGT 296
 QY 340 GTTTGCCCCACCCGGTGCACAGCAGGACACCAACCAATCACCAGTCAATGACGAACTTC 399
 Db 295 GCTGTCCCGCAGCAGTACATTTGGAGTCCACCACCTGCAGTACCAGTTTGCATCGGCCAC 236
 QY 400 TACCAGCACCCAGGAGTATACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCC 459
 Db 235 GACCTGAGGAGTCAAAAGTTCAATTTGGTCTTACCCCAATCCGTCGCAATTTAGTCCCG 176
 QY 460 TAGCGCATCAATGACCCACATTTGGGCTCGATCGAGACGTCGGGCGACCCCTATCGGGT 519
 Db 175 CCGGACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCGCCACTCC--AGGGCT 118
 QY 520 CGATGCCGCCCAACAGTATGACAGTGTGTTGGCGGTACCTCGATAGTAGACAGCATAA 579
 Db 117 TCGCGCAGCCACACCGGTGTAATACATTTGGT--TAGGATTTGGAATGTGGCGCTGTT 60
 QY 580 GTGAAAGTCAAAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAG 627
 Db 59 GCGGTGGAGATGACAAAAGTGGCGAAATATGAAAGTAGAGACCAAG 12

RESULT 14
 ADA68525/c
 ID ADA68525 standard; DNA; 735 BP.

XX AC ADA68525;
 XX DT 20-NOV-2003 (first entry)
 XX Arabidopsis thaliana gene, SEQ ID 566.
 DE Plant; bacterial infection; fungal infection; viral infection; ds.
 KW Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 XX WO2003000898-A1.
 XX 03-JAN-2003.
 XX 22-JUN-2001; 2001WO-IB001105.
 XX 22-JUN-2001; 2001WO-IB001105.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WP1; 2003-175290/17.
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 566; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;
 SQ Query Match 11.7%; Score 186.8; DS 7; Length 735;

Best Local Similarity 62.4%; Pred. No. 5.2e-32;
 Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;
 QY 46 GGTATCTTTTGTGAAAAAATTTGAAAAAGACGTAGGACCCACATG-----GACCTTGGG 99
 Db 586 GGCATCTCTGCTTAAAGAAATCTTGAGTACTCAGTATCGCTACATGATCCCTGACCGTTGC 527
 QY 100 TGCACATATTTGTTGCTCTCCAAATGTGGTACAAAGATTGTTACATCTCTCGGGTACTT 159
 Db 526 TACAACAGTATTGTTGCTCTGCTGAAATACAGTACAGGGTGTGTCATCCACCTCGGGGTC 467
 QY 160 TAAGCTGATAGGACATTCACCATTTATTTGCGTGCATTGAATTGTGGCAATTTCC 219
 Db 466 TCACACAGTTTGGACATTTGTCGTTTATGTCGGTACATAGTATCCGATGGCAGTTC- 408
 QY 220 CTCCTACTTGGATTAGTTCGGGGCGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAA 279
 Db 407 -----GACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGCAAGTGAGA 356
 QY 280 TGTCCACAGAAATCTAAGTTGTTGAACTGCTCCAGGGGTACTCGGCTAGGGTGTGTTGGTG 339
 Db 355 TATCGTAGAAGTCTAAGTTGTTGAAATTTGGTTCAAAGCGTACTCAGCCAACTGTTTGGTG 296
 QY 340 GTTTCCTCCACCCCGGTGCACTGCAGGACACCAACCAATCAATCCAGTCAATGACCAACCTC 399
 Db 295 GCTGTCCCGCCAGCCAGTACATTTGGAGTCCACCACTGCAGTACCAGTTTGGCATCGGCCAC 236
 QY 400 TACCAGCACCCAGGAGTATACATCCAGTACGACCCCATATACGTGCCATCGTACTGCCCC 459
 Db 235 GACCTGAGGAGTCAAAAGTTTCAATTTGGTCTACCCCAATCCGTGCCATTTAGTGCCCG 176
 QY 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGCGACCGCTATCGGGT 519
 Db 175 CCGCACATCTAGCTCCATGATTTGGCCAGCATCTAGACGTGCGCCACTCC--AGGGCT 118
 QY 520 CGATGCCGCCCAACAGTATGACAGTGTGTTGGCGGTACTCTGATAGTAGACAGCATAA 579
 Db 117 TCGCGCAGCCACACCGTGTAACTACATTTGGT--TAGGATTTGGAATGTGGCGCTGTT 60
 QY 580 GTGAAAGTCAAAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAG 627
 Db 59 GCGGTGGAGATGACAAAAGTGGCGAAATATGAAAGTAGAGACCAAG 12

RESULT 15
 ABN98566/c
 ID ABN98566 standard; DNA; 950 BP.

XX AC ABN98566;
 XX DT 01-AUG-2002 (first entry)
 XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 334.
 DE Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 KW disease; crop; thale cress; tolerance factor; insect; pathogen;
 KW nutrition; ds.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX US2002023281-A1.
 XX 21-FEB-2002.
 XX 26-JAN-2001; 2001US-00770445.
 XX 27-JAN-2000; 2000US-0178472P.
 XX (GORL) GORLACH J.
 XX (ANYI) AN Y.
 XX (HAM) HAMILTON C M.
 XX (PRIC) PRICE J L.
 XX (RAIN) RAINES T M.

PA (YUYU) YU Y.
PA (NAME) RAMEKA J G.
PA (PAGE) PAGE A.
PA (MATH) MATH A V.
PA (LEDF) LEDFORD B L.
PA (WESS) WESSNER J P.
PA (HAAS) HAAS W D.
PA (KRIC) KRICKER M.
PA (SLAT) SLATER T.
PA (DAVI) DAVIS K R.
PA (ALLE) ALLEN K.
PA (HOFF) HOFFMAN N.
PA (HURB) HURBAN P.
XX
PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Krickler M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2002-403163/43.
XX
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein.
XX
PS Claim 1; SEQ ID NO 334; 49pp + Sequence Listing; English.
XX
CC The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridizing under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful for
CC enhancing or inhibiting production of a biosynthetic product in a plant.
CC (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445
XX
SQ Sequence 950 BP; 261 A; 225 C; 213 G; 251 T; 0 U; 0 Other;

Query Match 11.7%; Score 186.8; DB 6; Length 950;
Best Local Similarity 62.4%; Pred. No. 5.5e-32;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;

QY 46 GGTATCTTTGTTGAAAAATTGGAAGAACGTAGGACCAATG-----GACCTTGGG 99
DB 594 GGCATCTCTGCTTAAGAATCTTGAGTACTCAGTACGTACATCCCTGACCGGTGCG 535

Search completed: August 18, 2004, 07:59:08
Job time : 574.22 secs

QY 100 TGCAACAATATTGTTGTCCTCCAAATGTCGTAAGGATGTTTACATCTCCGGGTACTT 159
DB 534 TACAACAGTATTGGTTGCTGTAATACAGTACACGGGTGTTTGCATCCACCTGGGGCTC 475
QY 160 TAGCTGACTAGGACATTCACCAATTTATATTTGCGGTGCATTGAATTGTTGGCATTTCC 219
DB 474 TCAACAGGTTTGACATTTGCTGTTTATGTCGCGGTACATAGTATCCGATGACATTC- 416
QY 220 CTCACCTTGGATTAGTCCGGGGGAAAGTTCATCGGTATATTAAATCCATCAACTTAAAGAA 279
DB 415 -----GAACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAAGTGAGA 364
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGTCCTCAAGCGGTACTCGGCTAGGGTGTGTTGGTG 339
DB 363 TATCGTAGAAGTCTAAGTTGTTGAATTGTTCAAAGCGGTACTCAGCAACGTGTTTGGTG 304
QY 340 GTTTGCCCCACCGCGTGCATGTCAGGACACCAACAATCACCAGTCAATGACGACGACCTC 399
DB 303 GCTGTCCCCCAGCAGTACATTGGAGTCCACACTGCAGTCACCAAGTTTGGCATCGGCCAC 244
QY 400 TACCAGACCCACGAAAGTTACATCCAGTAGAGAGCCCATATAGTGCATCGTAGTCCCCC 459
DB 243 GACCTGAGGAGTCAAAAGTTACAATTTGCTCTACCCCAAAATCCGTGCCATTTTAGTCCCG 184
QY 460 TAGGCGCATCAATGACCCACATTTGGCCTCGATCGAGACGTGGGGCACCGCCTATCGGCT 519
DB 183 CCGGACATCTAGCTTCCATGATTGGCCAGCATCTAGACGTGGGCCACCTCC--AGGGCT 126
QY 520 CGATCGCGCCCAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGACAGCATAA 579
DB 125 TGGGCGAGCCCAACACGCTGTAACTACATTTGGTT--TAGGATTTGGAATGTGGCGGTGTT 68
QY 580 GTCAAAAGTCAAAAACCCAGAGGGGAGAACCAAAAGAGAGATCTCAAG 627
DB 67 GCGGTGGAGATGAGCAAAAAGTCCGAAAAATATGAAAGTAGAGACCAAG 20

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 06:27:01 ; Search time 123.079 seconds
(without alignments)
7205.239 Million cell updates/sec

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Perfect score: 1598
Sequence: 1 gtaatacagactacatagg.....tggtgaagtgtggtttc 1598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	468.8	29.3	3033	1	US-08-482-037A-1
C 2	419.8	26.3	883	1	US-07-828-798C-4
C 3	419.8	26.3	883	2	US-08-315-868A-4
C 4	419.8	26.3	883	3	US-08-495-819B-4
C 5	419.8	26.3	884	1	US-07-828-798C-5
C 6	419.8	26.3	884	2	US-08-315-868A-5
C 7	419.8	26.3	884	3	US-08-495-819B-5
C 8	168.8	10.6	875	4	US-09-589-733C-4
C 9	144.8	9.1	900	1	US-08-181-271A-4
C 10	144.8	9.1	900	1	US-08-449-315-4
C 11	144.8	9.1	900	1	US-08-444-803-4
C 12	144.8	9.1	900	1	US-08-449-043-4
C 13	144.8	9.1	900	1	US-08-456-265A-4
C 14	144.8	9.1	900	1	US-08-456-416-4
C 15	144.8	9.1	900	1	US-08-455-244-4
C 16	144.8	9.1	900	1	US-08-454-876-4
C 17	144.8	9.1	900	2	US-08-457-384-4
C 18	144.8	9.1	900	2	US-08-456-262-4
C 19	144.8	9.1	900	2	US-08-456-240-4
C 20	144.8	9.1	900	2	US-08-455-736-4
C 21	144.8	9.1	900	2	US-08-971-217-4
C 22	144.8	9.1	900	3	US-09-350-600-4
C 23	144.8	9.1	900	4	US-09-906-234-4
C 24	138.6	8.7	910	4	US-09-685-292-1
C 25	109	6.8	894	1	US-08-178-708-7
C 26	109	6.8	894	1	US-08-457-552-7
C 27	109	6.8	894	1	US-08-456-430-7

C 28	109	6.8	894	2	US-08-994-418-7
C 29	109	6.8	894	5	PCT-US95-00432-7
C 30	90.8	5.7	1309	6	5221624-4
C 31	90.6	5.7	621	4	US-09-224-514A-9
C 32	89.2	5.6	621	4	US-09-224-514A-1
C 33	89.2	5.6	621	6	5221624-31
C 34	81.4	5.1	624	2	US-08-426-599B-3
C 35	75.2	4.7	624	2	US-08-426-599B-1
C 36	73.2	4.6	2051	1	US-08-482-037A-2
C 37	66.2	4.1	230	4	US-09-589-733C-28
C 38	57.8	3.6	640681	4	US-09-790-988-1
C 39	53.8	3.4	1924	4	US-09-424-283-5
C 40	52.6	3.3	640681	4	US-09-790-988-1
C 41	52	3.3	6583	4	US-10-204-708-25
C 42	51.4	3.2	388	4	US-09-598-401C-38
C 43	51.4	3.2	3095	6	5231168-1
C 44	49.6	3.1	6152	3	US-08-973-462-1
C 45	49.4	3.1	5152	4	US-10-204-708-74

ALIGNMENTS

RESULT 1
US-08-482-037A-1/c
; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Osmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Q. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,037A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,243
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/180,428
; FILING DATE: January 12, 1994
; APPLICATION NUMBER: 08/065,147
; FILING DATE: May 20, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Q. Henry
; REGISTRATION NUMBER: 28,309
; REFERENCE/DOCKET NUMBER: 7024-8/PUR16CIPDIVII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 634-3456
; TELEFAX: (317) 637-7561
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 bases
; TYPE: Nucleotide/Amino Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
; US-08-482-037A-1
Query Match 29.3%; Score 468.8; DB 1; Length 3033;

245 CAGCATTGAAGTTACAATTAGTAGCGGCCCATACACGTGCCATTTTATAGTCTGTTGGCG 186
466 CATCAATGACCCACATTTGGCTCGATCGAGCGTGGGACCGCCTATCGG-GTCGATG 524
185 CATTAATGACCCCAAGTTTGGCTCGATCGAGCGCGCGGCACCGCCTATGGGTGCGACG 126
525 CCGGCCAAAACGATGTAGGACAGTTTGGCGGTACCTCGATAGTGACAGCATAGTGAA 584
125 CCGGCCAAAACGTTGACGACAGTTTGT--TCGGACCTCGATAGTGGCAGCATAGTATA 68
585 AGTCACAAAACGAGGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGT 637
67 AGTCACCAAGCAAGGAGGAGAACCAAAAGAGATCTCAAGTTGCCCATGT 15

RESULT 3
US-08-315-868A-4/c
; Sequence 4, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/POCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-08-315-868A-4
Query Match 26.3%; Score 419.8; DB 2; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;

Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;
QY 46 GGTATCTTTGTTGAAAAAATTGGAAGAAAGAGTGGAGCCACATGACCTTGGGTGCAAC 105
DB 605 GCACTCTTTGTTGAAAAAATTGGAAGAAAGTGGAGCCACAGGTCTTGTGTGCAAC 546
QY 106 AATATTGTTGCTCTCCAAATGTGTCACAGGATTTTACATCTCTCGGGTACTTTAAGT 165
DB 545 AATATTGTTGCTCTCCAAATGTGTCACAGGATTTTACATCTCTCGGGTACTTTAAGT 486
QY 166 GACTAGGACATTCACCATTTATATTGCGGTGCATTTGAATTTGTGGCATTTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGGTTTATATTAGCGGTACATGAATTCGATGGCATTTCCCTCCAC 426
QY 226 TTGGATTAGTCTGGGGCGAAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 285
DB 425 TAGGGTTAGTCTGGGGCGAAAAGTCACTCGGTATATTAAATCCATCAACTAAAGAAATGTCCC 366
QY 286 AGAATCTTAAGTTGTTGAATCTGTCACAGGCGTACTCGGCTAGGTTGTTGTTGTTGCG 345
DB 365 AGAATCTTAAGTTGTTGAATCTGTCACAGGCGTACTCGGCTAGGTTGTTGTTGTTGCG 306
QY 346 CCACCCCGGTGCACTGACGAGCACACCAACATACCATCATGACGAACTTACCCAG 405
DB 305 CCACCCCGGTGCACTGACGAGCACACCAACATACCATCATGACGAACTTACCCAG 246
QY 406 CACCCCGGTGCACTGACGAGCACACCAACATACCATCATGACGAACTTACCCAG 465
DB 245 CAGCATTTAAGTTTACAAATTTAGTACGCGCCCATACACGTCCTTTTAGTACCTCGTGGCG 186
QY 466 CATCAATGACCCACATTTTGGCTCGATCGAGACGTCGCGGCACCGCTATCGG-GTCGATG 524
DB 185 CATTAATGACCCCAAGTTTGGCTCGATCGAGACGTCGCGGCACCGCTATCGGTTGCGAG 126
QY 525 CCGCCCAAAACGATGTAGGACAGTTTGGCTCGATCGAGACGTCGCGGCACCGCTATCGGTTGCGAG 584
DB 125 CCGCCCAAAACGTTGACGACAGTTTGT--TCGGACCTCGATAGTGGCAGCATAGTATA 68
QY 585 AGTCACAAAACGAGGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGT 637
DB 67 AGTCACCAAGCAAGGAGGAGAACCAAAAGAGATCTCAAGTTGCCCATGT 15

RESULT 4

US-08-495-819B-4/c
; Sequence 4, Application US/08495819B
; Patent No. 6087161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,819B
; FILING DATE: 31-MAY-1995

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: 30086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-4

Query Match 26.3%; Score 419.8; DB 3; Length 883;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAAAAGACGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAAAAAATTTGAGAACCAATGTAGAACCAAGGTCCTTGTGTGCAAC 546

QY 106 AATATTGTTGCTCCAAATGTGTGTACAAAGATTGTGTACATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCGAATGTGTGTACAAAGGTTATTACATCTCCGGGACCACTTAAGTT 486

QY 166 GACTAGGACATTCACCATTTTATTTTCCGTGCAATTGAATTTGTGGCATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGGTTTATTTAGCCGTACAAATGAATTCGATGCAATTCCTCCAC 426

QY 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCC 285
DB 425 TAGGTTAGTCGGGGCGAAAGTCATCGGTATATTGAATTCATCAACTAAAGAAATGTCC 366

QY 346 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCAAGCAGACCTTACCAG 405
DB 305 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCAAGCAGTACCCCTACCAG 246

QY 406 CACCACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCTGATGCCCCTAGGG 465
DB 245 CAGCATTTGAAGTTACATTTAGTACGGCCCATACACGTGCAATTTTAGTACCTCTGGG 186

QY 466 CATCATGACCCCATTTGGCCTCGATCGAGAGTGTGGGACCCGCTATCGG-GTCAATG 524
DB 185 CATTGATCACCAGTTTGGCCTCGATCGAGAGTGTGGGACCCGCTATGGGTGTGCAAG 126

QY 525 CCGCCCAACAGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGACAGCATTAAGTAA 584
DB 125 CCGCCCAACAGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGAGCAGCATTAAGTAA 68

QY 585 AGTCACAAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
DB 67 AGTCACAAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 15

; RESULT 5
; US-07-828-798C-5/c
; Sequence 5, Application US/07828798C
; Patent No. 5389609
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,798C
; FILING DATE: 06-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-07-828-798C-5

Query Match 26.3%; Score 419.8; DB 1; Length 884;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAAAAGACGTAGGACACACATGGACCTTGGGTGCAAC 105
DB 605 GGCATCTTTGTTGAAAAAATTTGAAAAAATTTGAGAACCAATGTAGAACCAAGGTCCTTGTGTGCAAC 546

QY 106 AATATTGTTGCTCCAAATGTGTGTACAAAGATTGTGTACATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCGAATGTGTGTACAAAGGTTATTACATCTCCGGGACCACTTAAGTT 486

QY 166 GACTAGGACATTCACCATTTTATTTTCCGTGCAATTGAATTTGTGGCATTTCCCTCCAC 225
DB 485 CGCGGGGACATTCGCGGTTTATTTAGCCGTACAAATGAATTCGATGCAATTCCTCCAC 426

QY 226 TTGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCC 285
DB 425 TAGGTTAGTCGGGGCGAAAGTCATCGGTATATTGAATTCATCAACTAAAGAAATGTCC 366

QY 346 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCAAGCAGACCTTACCAG 405
DB 305 CCCACCCGGTGCATCTGAGGACACCAACCAATCACCAGTCAAGCAGTACCCCTACCAG 246

QY 406 CACCACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCTGATGCCCCTAGGG 465
DB 245 CAGCATTTGAAGTTACATTTAGTACGGCCCATACACGTGCAATTTTAGTACCTCTGGG 186

QY 466 CATCATGACCCCATTTGGCCTCGATCGAGAGTGTGGGACCCGCTATCGG-GTCAATG 524
DB 185 CATTGATCACCAGTTTGGCCTCGATCGAGAGTGTGGGACCCGCTATGGGTGTGCAAG 126

QY 525 CCGCCCAACAGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGACAGCATTAAGTAA 584
DB 125 CCGCCCAACAGTATGAGCAGTTGTTGGCGGTACCTCGATAGTGAGCAGCATTAAGTAA 68

QY 585 AGTCACAAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
DB 67 AGTCACAAAAGCCAGAGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 15
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Qy 286 ABAATCTAAGTCTTGAAGTCCAGGGTACTCGGTAGGTTGTTGGTGGTTTC 345
Db 365 AGAATCTAAACCACTGAATGGTCCAAAGCGTATTGAGCAAGGTGTTGGTGGTTAC 306
Qy 346 CCCACCGGTGCACTGAGGACACACCAATCACCAGTATGACGAACTCTACCA 405
Db 305 CCCACCGGTGCACTGAGGACACACCAATCACCAGTATGAGCAAGGTGTTGGTGGTTAC 246
Qy 406 CACACCGAAGTATACATCCAGTACGACCCCATATAGTGCATGTCCTAGGCG 465
Db 245 CAGCATTGAAGTTCAATAGTACGCGCCCATACACGTGCATTTTAGTACCTCGTGGCG 186
Qy 466 CATCAATGACCCATTTGGCTCGATCGAGACGTCGGGACCCGCTATCGG-GTCCATG 524
Db 185 CATGATCACCAAGTTTGGCTCGATCGAGACGTCGGGACCCGCTATGAGTGGTGGACG 126
Qy 525 CCGGCCAAACGATGTATGAGCAGTTTGGCGGTACCTCGATGACAGCATAGTGAA 584
Db 125 CCGGCCAAACGATGTATGAGCAGTTTGGCGGTACCTCGATGACAGCATAGTGAA 68
Qy 585 AGTCACAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
Db 67 AGTCACAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 15

```

RESULT 6

US-08-315-868A-5/c
Sequence 5, Application US/08315868A
Patent No. 5856151

GENERAL INFORMATION:

APPLICANT: Woloshuk, Charles P.
APPLICANT: Melchers, Leo S.
APPLICANT: Cornelissen, Bernardus J. C.
APPLICANT: Meulenhoff, Elisabeth J. S.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Van Den Elzen, Petrus J. M.
TITLE OF INVENTION: Antifungal Preparations, Process for
TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
TITLE OF INVENTION: Decreased Susceptibility to Fungi
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/315,868A

FILING DATE: 09-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/828,798

FILING DATE: 06-APR-1992

APPLICATION NUMBER: PCT/NL91/00089

FILING DATE: 31-05-91

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30086

REFERENCE/DOCKET NUMBER: U-8622-6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

TELEFAX: (212) 246-8959

TELEX: 233288

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 884

TYPE: Nucleotide
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
US-08-315-868A-5

Query Match 26.3%; Score 419.8; DB 2; Length 884;
Best Local Similarity 84.0%; Pred No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

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Qy 46 GGTATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCAATGAGCCTTGGGTGCAAC 105
Db 605 GGCATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCAATGAGCCTTGGGTGCAAC 546
Qy 106 AATATTTGTTCTCTCCAAATGTTGACAGGATTTGATCATCTCGGTGATCTTTAAGT 165
Db 545 AATATTTGTTCTCTCCAAATGTTGACAGGATTTGATCATCTCGGTGATCTTTAAGT 486
Qy 166 GACTAGGACATTCACCATTTATATTTGCGGTGCATTTGAATTTGTGGCATTTCCCTCCAC 225
Db 485 CGCGGGACATTCGCGGTTTATATTAGCGGTACATGAATTCATGGCATTTCCCTCCAC 426
Qy 226 TTGGATTAGTCGGGGGAAAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCC 285
Db 425 TAGGGTTAGTCGGGGGAAAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCC 366
Qy 286 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGCTAGGGTGTGTTGGTGGTTGC 345
Db 365 AGAATCTAAGTTGTTGAACTGTTCCAGGCGTACTCGGCTAGGGTGTGTTGGTGGTTGC 306
Qy 346 CCACCCGGTGCACTGACGAGACACCAACATACCAATACCAAGTATGACGACCACTTACCAAG 405
Db 305 CCACCCGGTGCACTGACGAGACACCAACATACCAATACCAAGTATGACGACCACTTACCAAG 246
Qy 406 CACACCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGGCCCTTAGGGCG 465
Db 245 CACATTTAAGTTACATTTAGTACGCGCCCATATAGTGCATCGTAGGCCCTTAGGGCG 186
Qy 466 CATCAATGACCCCAATTTGGCTCGATCGAGACGTCGGGACCCGCTATCGG-GTCCATG 524
Db 185 CATGATCACCAAGTTTGGCTCGATCGAGACGTCGGGACCCGCTATCGG-GTCCATG 126
Qy 525 CCGGCCAAACGATGTATGAGCAGTTTGGCGGTACCTCGATGACAGCATAGTGAA 584
Db 125 CCGGCCAAACGATGTATGAGCAGTTTGGCGGTACCTCGATGACAGCATAGTGAA 68
Qy 585 AGTCACAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 637
Db 67 AGTCACAAAGCCAGAGGAGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGT 15

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RESULT 7

US-08-495-819B-5/c
Sequence 5, Application US/08495819B
Patent No. 6087161

GENERAL INFORMATION:

APPLICANT: Woloshuk, Charles P.
APPLICANT: Melchers, Leo S.
APPLICANT: Cornelissen, Bernardus J. C.
APPLICANT: Meulenhoff, Elisabeth J. S.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Van Den Elzen, Petrus J. M.
TITLE OF INVENTION: Antifungal Preparations, Process for
TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
TITLE OF INVENTION: with Decreased Susceptibility to Fungi
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York

```

; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,819B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-010255-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-5

Query Match 26.3%; Score 419.8; DB 3; Length 884;
Best Local Similarity 84.0%; Pred. No. 6.8e-96;
Matches 498; Conservative 0; Mismatches 92; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAATTTGAAAAAGACGTAGACACACATGGACCTTGGTGGCAAC 105
DB 605 GGCATCTTTGTTGAAAAATTTGAAAAAATGTAGACACACAGGTCTTTGTGTCAAC 546
QY 106 AATATTGTTGCTCCCAAAATGTGTACAAGATTGTTACATCTCCGGGTACTTTAAGCT 165
DB 545 AATATTGTTGCTCCCAAAATGTGTACAAGATTGTTACATCTCCGGGTACTTTAAGCT 165
QY 166 GACTPAGACATTCACATTTATTTTCCCGTGCATGAATTTGTGGCAATTTCCCTCCAC 225
DB 485 CGCGGGACATTCGCGTTTATTTAGCCCGTACAATGAATTTGCATGCGCATTTCCCTCCAC 426
QY 226 TTGATTTAGTCGGCGGAAAGTCACTCGGTATATTAATCCATCACTAAGAAATGTCCT 285
DB 425 TAGGGTTAGTCGGCGGAAAGTCACTCGGTATATTAATCCATCACTAAGAAATGTCCT 366
QY 286 AGAAATCTAAGTTGTTGAACTGTGTCCAAAGCGTACTCGGGTAGGGTGTGTTGTTGC 345
DB 365 AGAAATCTAAGTTGTTGAACTGTGTCCAAAGCGTACTCGGGTAGGGTGTGTTGTTGC 306
QY 346 CCCACCGGTGCACTGACGACACACCAACATCACTGATGATGACGAACTCTACCAAG 405
DB 305 CCCACCGGTGCACTGATGATGACGACACCAACATCACTGATGATGACGAACTCTACCAAG 405
QY 406 CACCAACGAAAGTTACATCCAGTACGACCCCATATACGTGCACTGATGACCCCTAGGGG 465
DB 245 CAGCATTGAAGTTACATTTAGTAGCGGCCCATACACGTCGCAATTTTAGTACCTGCGG 186
QY 466 CATCAATGACCCCATTTGGCCCTCGATTCGAGACGTGCGGACCGCCCTATCGG-GTCGATG 524
DB 163 TTAAGACCCAGGTTTGGCCCTCGATTTAAGTTTGTGGCGCCGCCACC--AGGCCCCGCCAGC 106

; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,819B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/315,868
; FILING DATE: 30-SEPT-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APRIL-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-010255-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-495-819B-5

Query Match 10.6%; Score 168.8; DB 4; Length 875;
Best Local Similarity 61.3%; Pred. No. 5.9e-33;
Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;

QY 49 ATCTTTGTTTGAATAATTTGAAAAAGACGTAGACACACATGGACCTTGGGTGCAACAT 108
DB 577 ATCTGGTCTTGAATAATTTGATAATTCAGTTGGTCCACATTTTCCAGAGTTGCAACAT 518
QY 109 ATTGTTGCTCCAAATGTGTACAAGATTGTTTACATCTCTCCGGGTACTTTAAGCTGAC 168
DB 517 ACTGATCAGTTTGTACACGGTGCAGGGTTATTGACCCGCCAGAGCCCGTAACAC 458
QY 169 TAGGACATTCACATTTATTTTCCCGTGCATTTGAATTTGTGTGGCATTTCCCTCCACTT 228
DB 457 CAGGACACTGGCCATTGATATCCGAGTACATGAGATACCCCGGTGCAACCC-----AT 404
QY 229 GATTAGTCGGCGGAAAGTCACTCGGTATTTAATCCATCACTAATAAGAAATGTCACAGA 288
DB 403 TAGAATTTGGTCTTAACACCATCGGCATTTGAATTCGTCCCAAGAGAAATGTCANAAG 344
QY 289 AATCTAAGTTTGTGAACCTGTTCCAAAGCGTACTCGGGTAGGGTGTGTTGGTGGTTGCCCC 348
DB 343 AATCAAGATTGTTGAACCTGTTTCAAGCGTACTCGGCCAATGTTGTTGGTGGGTACCAT 284
QY 349 ACCCGGTGCACTGACGACACCAACCAATCACCAGTATGACGAACTCTACCAACAC 408
DB 283 AGTTTGGCATTTGAGGAGACCGTTTGAATCACCAGTCTGACACCTCGCTCGCCAGAAC 224
QY 409 CACGAAATTCATCCAGTACGACCCCATATACGTGCACTGATGTCCTAGTCCCTAGGCCCAT 468
DB 223 CATCAAGTTGCAATTTGTTTCGGGGCCATATACGGGTCTCTGCTGTGCCAGCTGCGACGG 164
QY 469 CAATGACCCCATTTGGCTCGATCGAGACGTGCGGACCGCCCTATCGGGTCGATCGCGC 528
DB 163 TTAAGACCCAGGTTTGGCCCTCGATTTAAGTTTGTGGCGCCGCCACC--AGGCCCCGCCAGC 106

; US-09-589-733C-4/c
; Sequence 4, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
; US-09-589-733C-4

Query Match 10.6%; Score 168.8; DB 4; Length 875;
Best Local Similarity 61.3%; Pred. No. 5.9e-33;
Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;

QY 49 ATCTTTGTTTGAATAATTTGAAAAAGACGTAGACACACATGGACCTTGGGTGCAACAT 108
DB 577 ATCTGGTCTTGAATAATTTGATAATTCAGTTGGTCCACATTTTCCAGAGTTGCAACAT 518
QY 109 ATTGTTGCTCCAAATGTGTACAAGATTGTTTACATCTCTCCGGGTACTTTAAGCTGAC 168
DB 517 ACTGATCAGTTTGTACACGGTGCAGGGTTATTGACCCGCCAGAGCCCGTAACAC 458
QY 169 TAGGACATTCACATTTATTTTCCCGTGCATTTGAATTTGTGTGGCATTTCCCTCCACTT 228
DB 457 CAGGACACTGGCCATTGATATCCGAGTACATGAGATACCCCGGTGCAACCC-----AT 404
QY 229 GATTAGTCGGCGGAAAGTCACTCGGTATTTAATCCATCACTAATAAGAAATGTCACAGA 288
DB 403 TAGAATTTGGTCTTAACACCATCGGCATTTGAATTCGTCCCAAGAGAAATGTCANAAG 344
QY 289 AATCTAAGTTTGTGAACCTGTTCCAAAGCGTACTCGGGTAGGGTGTGTTGGTGGTTGCCCC 348
DB 343 AATCAAGATTGTTGAACCTGTTTCAAGCGTACTCGGCCAATGTTGTTGGTGGGTACCAT 284
QY 349 ACCCGGTGCACTGACGACACCAACCAATCACCAGTATGACGAACTCTACCAACAC 408
DB 283 AGTTTGGCATTTGAGGAGACCGTTTGAATCACCAGTCTGACACCTCGCTCGCCAGAAC 224
QY 409 CACGAAATTCATCCAGTACGACCCCATATACGTGCACTGATGTCCTAGTCCCTAGGCCCAT 468
DB 223 CATCAAGTTGCAATTTGTTTCGGGGCCATATACGGGTCTCTGCTGTGCCAGCTGCGACGG 164
QY 469 CAATGACCCCATTTGGCTCGATCGAGACGTGCGGACCGCCCTATCGGGTCGATCGCGC 528
DB 163 TTAAGACCCAGGTTTGGCCCTCGATTTAAGTTTGTGGCGCCGCCACC--AGGCCCCGCCAGC 106
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QY 529 CCAACGATGATGACAGTTGTT 552
Db 105 CCAACGATGATGACAGTTGTT 82

RESULT 9

US-08-181-271A-4/c
; Sequence 4, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,271A
; FILING DATE: 13-JAN-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/COC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-181-271A-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
QY 45 GGTATCTTTGTTGAAAATTTGAAAGAGTAGGACCAT-----GCACCTTGGG 99
Db 607 GGCATCTTTCTTAAATAATCTGCACAAATAGTAGGCCCATGATCCAGGCCCATTTG 548
QY 100 TGCACAAATATTGTTGCTCCTCCAATGTGGTACAAAGGATTTTACATCTCCGGGTACTT 159
Db 547 TACACAAATATTCAITTTGTTTATACAGATACATGGGTTTGTACATCCACCTTGTGTTT 488
QY 160 TAACTGTAGTACGACATTCACCATTTATTTTGGCGTGCATGAATTGTGTGCATTTCC 219
Db 487 TCAACTGTGTCTGGGCATTTGTTGTTTAAATAGGTGCTGTGCATCTGAGATTACGACAT 432
QY 220 CTCCACTTGGATTAGTCGGGGGCGAAAGTCATCGGTATATTTAAATCCATCAACTAAAGAA 279
Db 431 -----CTTCCATTGGTCCGGCTGAATTCATGGGATGTTAATCCATCAAGAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTTTGAATGTTTCAAGCGCTACTCGGCTAGGGTGTGTTGGTG 339
Db 376 TGTGACAAAGTC---CTGATTTGGGTTGATTAAAGTGCATAATTCAGTAAAGTGTAGGTG 320
QY 340 GTTTGCCCCCGGTGTCATGACGACACACCAATCACCAGTCATGACGACCTC 399
Db 319 CTTTCCATAGCCTTGACACTCTTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
QY 400 TACCAGCACCCAGAGTTTACATCCAGTACGACCCCATATAGTGCATCTAGTGCCCC 459
Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAATTCGAGCTGTGCTTCTCTG 200
QY 460 TAGGCGCATCATGACCCACATTTGSCCTCGATCGAGAGCTGGGACCGCCTATCGGTT 519
Db 199 GGTTCATTAATGCTTCCAAAGATTGGCCTGAGTCGAGCGCCTGCTCCACC--TGGAGA 142
QY 520 CGATGCGGCCCAACCGATGTGTGACAGTTGTTGGCGGTACCTCGATATAGTACGACATAA 579
Db 141 GGCCGGCGCCAGACTGTGTAGTGATTTGTTGAC--NATGTCAAAAGTGGCAGCATGA 84
QY 580 GTGAAAGTCACAAA 593

Db 83 GTACAGCTACAAA 70
RESULT 10
US-08-449-315-4/c
; Sequence 4, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-449-315-4
Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
QY 46 GGTATCTTTTGGAAAAATGGAAAAAGACGTAGGACACAT-----GGACCTTGGG 99
Db 607 GGCATCTTTTCCTTAAAAAATCTCGACAAATCAGTAGGCCACCATGATCCAGGCCATTG 548
QY 100 TGCACATATATTGTCTCTCAATGGTGTACAGGATTGTGTACATCTCCCGGTACTT 159
Db 547 TACACATATATTCATTTGTTTATCAGTACATGGTGTGTACATCCACCTTGTGTTT 488
QY 160 TAAGCTGCTAGGACATTCACATTTATTTATTCGCTGCAATTTGAATTTGTGTGCAATTTCC 219
Db 487 TCAACTGTGCTGGGCATTTGTTTAAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCGGGCGGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAA 279
Db 431 -----CTTCCATTTGTCGGCTGAAATTCATGGGGATGTTAAATCCATCAAGAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTGAACTGGTCCAGGGGTACTCGGCTAGGGTGTTCGGTG 339
Db 376 TGTCGACAAAGTC--CTGATTGGTTGATTAAAGTCAAAATTCAGCTAAAGTGTAGGTG 320
QY 340 GTTTGCCCCACCGGTGCTGCTGAGGACACCAACATCACCATGTCATGCACGAACCTC 399
Db 319 CTTTTCATAGCCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCAATTAACCTC 260
QY 400 TACCAGCACACCGAAGTTACATCCAGTAGGACCCCATATACGTGCCATCGTAGTGCCC 459
Db 259 GGCCACTGCCATCGAAGTTGCAATTTGTTCCAGCCCAATGCGAGCTTGGACTGTTCTG 200
QY 460 TAGGGGATCAATGACCCCATTTGGCTCGATGAGACCTGCGGGACCCGCCCTATCGGT 519
Db 199 GGTTCACATTAATGCTCCAAAGATTGGCTGAGTCGAGCGCCCTGCCCTCCACC--TGAGA 142
QY 520 CGATGCCGCCCAACAGATGTATGGACAGTTGTTGGCGGTACCTCGATGTAGTACAGATAA 579
Db 141 GGCCGCCGCCAGACTGTGTAGGTGCATTTGTTGAC--AATGTCAAAAGTGGCAGATGA 84
QY 580 GTGAAAGTCAAAA 593

DB 83 GTACAGCTACAAA 70

RESULT 11

US-08-444-803-4/c

; Sequence 4, Application US/08444803

; Patent No. 5654414

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/444,803

; FILING DATE: 19-MAY-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT 1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/580,431

FILING DATE: 7-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 900 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-08-444-803-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;

Best Local Similarity 60.5%; Pred. No. 6.2e-27;

Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

QY 46 GGTATCTTTGTTGAAAAAATGGAAGAAAGTAGGACCAAT-----GGACCTTGGG 99

DB 607 GGCATCTTTCTTAAAAATCTCGAANAATCAGTAGGCCACATGATCCAGGCCCATTTG 548

QY 100 TGCAACAATATTGTTGCTCTCCAAATGTGGTACAGGATTTGTACATCTCCGGGTACTTT 159

DB 547 TACACAAATATTCAATGGTTTTTATCACAGTACATGGGTTGTACATCCACCTTGTGTTT 488

QY 160 TAAGCTGACTAGGACATTCACCAATTTATTTGGCGTGCAATTTGAATTTGTGTCATTTCC 219

DB 487 TCACCTGTCTGGCAATTTGTTGTTAATAGGTGCTGTGCACTCTGAGATTACACAT---- 432

QY 220 CTCACCTTGGATTAGTCGGGGGAAAGTCAATCGGTATATTAATCCATCAACTAAAGAAA 279

DB 431 -----CCTCCATTTGGTCCGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGAGA 377

QY 280 TGTCCCAAGAAATCTAAGTTGTTGAATGTTGTTCAAGGCGTACTCGGCTAGGTTGTTGTTG 339

DB 376 TGTCCCAAGAAATCTAAGTTGTTGAATGTTGTTCAAGGCGTACTCGGCTAGGTTGTTGTTG 320

QY 340 GTTTGCCCCCAACCGGTGCACTGCGAGACACACCAATCAGCAGTCAATGCGACACCTC 399

DB 319 CTTTCCATAGCTTGCACACTCTAAATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260

QY 400 TACCAGCACACCGAAGTTTACATCCAGTACAGACCCCATATAGTGCATTCGTAGTCCCTC 459

DB 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCGACCCCAATGCGAGCTCGACTGTTCTG 200

QY 460 TAGGGCATCAATGACCCCAATTTGGCTTCGATCGAGAGCTCGGGCACCGCTTATCGGGT 519

DB 199 GGTTCACATTAATGCTTCAAGATTGGCTGAGTGGCGCTGCTCCACC--TGGAGA 142

QY 520 CGATGCCGCCCAACGATGATGGAAGTTGTTGGCGGTACTTCGATAGTACAGCATAA 579

DB 141 GGCCCGGCCGACACTGTGTAGTGCAATTTGTTGAC--AATGTCAAAAGTGGCAGCATGA 84

QY 580 GTGAAAGTCACAAA 593

Db 83 GTAACAGCTACAAA 70
 RESULT 12
 US-08-449-043-4/C
 ; Sequence 4, Application US/08449043
 ; Patent No. 5689044
 ; GENERAL INFORMATION:
 ; APPLICANT: Ryals, John A.
 ; APPLICANT: Alexander, Danny C.
 ; APPLICANT: Beck, James J.
 ; APPLICANT: Duesing, John H.
 ; APPLICANT: Friedrich, Leslie B.
 ; APPLICANT: Goodman, Robert M.
 ; APPLICANT: Harms, Christian
 ; APPLICANT: Meins, Jr., Frederick
 ; APPLICANT: Montoya, Alice
 ; APPLICANT: Moyer, Mary B.
 ; APPLICANT: Neuhaus, Jean-Marc
 ; APPLICANT: Payne, George B.
 ; APPLICANT: Sperison, Christoph
 ; APPLICANT: Stinson, Jeffrey R.
 ; APPLICANT: Uknes, Scott J.
 ; APPLICANT: Ward, Eric R.
 ; APPLICANT: Williams, Shericca C.
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CIBA-GEIGY Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/449,043
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/181,271
 ; FILING DATE: 13-JAN-94
 ; APPLICATION NUMBER: US 08/093,301
 ; FILING DATE: 16-JUL-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,197
 ; FILING DATE: 6-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/678,378
 ; FILING DATE: 1-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/305,566
 ; FILING DATE: 6-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/165,667
 ; FILING DATE: 8-MAR-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/042,847
 ; FILING DATE: 6-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/632,441
 ; FILING DATE: 21-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/425,504
 ; FILING DATE: 20-OCT 1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/768,122
 ; FILING DATE: 27-SEP-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/580,431
 ; FILING DATE: 7-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/368,672
 ; FILING DATE: 20-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/329,018
 ; FILING DATE: 24-MAR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/045,957
 ; FILING DATE: 12-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elmer, James Scott
 ; REGISTRATION NUMBER: 36,129
 ; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919)541-8614
 ; TELEFAX: (919)541-8689
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 900 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-449-043-4

 Query Match 9.1%; Score 144.8; DB 1; Length 900;
 Best Local Similarity 60.5%; Pred. No. 6.2e-27;
 Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

 QY 46 GGTATCTTTTGTGAAAAAATGGAAAAAGACGTAGGACCAACAT-----GGACCTTGGG 99
 Db 607 GGCATCTTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACACATGATCCAGGCCCAATTG 548
 QY 100 TGCAACAATATGTCTCTCAAAATGGTACAGGATGTTTACATCTCTCCGGTACTT 159
 Db 547 TACACAATATTCATTTGTTTTTATCACAGTACATGGGTTGTTACATCCACCTTGTGTT 488
 QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGGTGCATTGAATTTGTGGCATTTCC 219
 Db 487 TCACTGTGCTGGGCATTTGTTGTTAATAGTGTCTGTCATCTGAGATTACGACAT---- 432
 QY 220 CTCCACTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAATTCATCAACTAAAGAAA 279
 Db 431 -----CTCCATTTGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGA 377
 QY 280 TGTCCCAAGAAATCTAAGTTGTTGAACCTGGTCCAAAGGGTACTCGGCTAGGTTGTTGGTG 339
 Db 376 TGTCCAGAAAGTC---CTGATGGGTTGATTAAGTGCAATTCAGCTAAAGTGTAGGTG 320
 QY 340 GTTTGCCCCACCCGGTGCACCTGCAGGACACACCAACATCAACAGTCATGCACCACTC 399
 Db 319 CTTTTCATAGCCTTGACACTCTAACATCCCGTTACAGTCTCCAGTCTCAAAATTAACCTC 260
 QY 400 TACCAGACACCCAGGATTTACATCCAGTACACCCCATATACGTGCCATCGTAGTGCCC 459
 Db 259 GGCCACTGCCATCGAAGTTGCAATTTGGTTTCACCCCAATGCGAGCTGGACTGTTCTTG 200
 QY 460 TAGGCGCATCAATGACCCACACATTTGGCCTCCATCGAGACGTTCGGGCGACCGCTATCGGGT 519
 Db 199 GGTTCACATTAATGCTCCAGATTTGGCTGAGTCGAGCCGCTGCCCTCCACC--TGGAGA 142
 QY 520 CGATGCCGCCCAAGCATGTATGACAGATTTGTTGGCGGTACCTCGATGATGACAGCAATA 579
 Db 141 GCGCGCGGCCAGACTGTGTAGGTGCATTTTGTGTAC--AATGTCAAAAGTGGCAGCATGA 84
 QY 580 GTGAAAGTCACAAA 593

Db 83 GTACACAGCTACAAA 70

RESULT 13

US-08-456-265A-4/c
; Sequence 4, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
; FILING DATE: 31-MAY-95

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-456-265A-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
QY 46 GGTATCTTTTGTGAAAAATTGGAAGAAAGCTAGGACACAT-----GGACCTTGGG 99
Db 607 GGCATCTTTCTTAAAAAATCTCGAAAAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
QY 100 TGCAACAATATTGTTCTCTCCAAATGTGGTACAAAGATTGTTCATCTCTCGGGTACTT 159
Db 547 TACAACAATATTGTTGGTTTTTATCAGATGATACGGTTGTTTACATCCACCTTGTGTTT 488
QY 160 TAAGCTGACTAGGACATTCACCAATTATATTTTGGCCGTGCAATTGAATTGTGGCATTTCC 219
Db 487 TCAACTGTCTGGGCATTGTTCTTAATAGGTGCTGTGCATCTGAGATTACGACAT---- 432
QY 220 CTCCACTTGGATTAGTCCGGGGGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAA 279
Db 431 -----CTCATTTGGTGGGCTGAATTCATGGGGAATGTTAAATCCATCAACAGAGAGA 377
QY 280 TGTCACAGAAATCTAAGTTTGTGAATCGTCCAAAGCGTACTCGGTGGGTGTTTGGTG 339
Db 376 TGTCGACAAAGTC--CTGATTGGGTGTTGTTAAGTCAAAATTCAGCTAAAGTTAGGTG 320
QY 340 GTTTGGCCACCCCGGTGCACTGACGACACACACCACCAATCACCAGTCATGCGAACCTC 399
Db 319 CTTTTCATAGCCTTCGACACTCTTAACATCCCGTTACAGTCTCCAGTCTCACAAATTACCTC 260
QY 400 TACCAGCACACCCAAAGTTACATCCAGTAGCAGCCCATATAGTGCCATCGTAGTCCCCC 459
Db 259 GGCACTGCAATCGAAGTTGCAATTGTTTCGACCCCAATCGAGGCTGGACTGTTCTTG 200
QY 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGAGCTGGGACCGCCTATCGGGT 519
Db 199 GGTTCACATTAATGCTCCAAAGATTGGCTGAGTCGAGCGCGCTGCCCTCCACC--TGGAGA 142
QY 520 CGATGCGGCCCAACGATGTATGACAGTTGTTGGCGGTACCTTCGATAGTGACAGCATAA 579
Db 141 GGCCGGGCCCAAGACTGTGTAGTGCAATTGTTTGAC--ATGTCAAAAGTGGCAGCATGA 84
QY 580 GTGAAAAGTCACAAA 593
Db 83 GTAACAGCTACAAA 70

RESULT 14

US-08-455-416-4/c
; Sequence 4, Application US/08455416
; Patent No. 577200
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-416-4
Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;
QY 46 GGTATCTTTTGTGAAAAAATTTGAAAAAGACGTAGGACACACAT-----GGACCTTGGG 99
Db 607 GCATCTTTTCTTAAAAAATCTCGACAATCAGTAGGCCACATGATCCAGGCCCATTTG 548
QY 100 TGCACAATATTGTTGCTCTCAATGTTGACAAAGATTGTTACATCTCTCGGGTACTT 159
Db 547 TACAACAATATTGTTGTTTATTCACAGTACATGGGTTGTTACATCCACCTTGTGTT 488
QY 160 TAAGCTGACTAGGACATTCACCATTTATTTGCGTGCATTGATTTGTTGGCATTTCC 219
Db 487 TCAACTGTGCTGGGCATTTGTTGTTTAAAGTGTGTCATCTGAGATTACGACAT---- 432
QY 220 CTCACATTTGGATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAA 279
Db 431 -----CCTCCATTTGGTGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGAGA 377
QY 280 TGTCCAGAAATCTAAGTTGTTGAACTGGTCCAGGGGTACTCGGTAGGGTGTGTTGGTG 339
Db 376 TGTCCAGAAAGTC---CTGATTGGGTTGATTAAAGTGCAAATTCAGCTAAAGTGTAGGTG 320
QY 340 GTTTCGCCCCACCCGGTGCATCTGCAGGACACCAACAATCAACAGTCATGACGAACTC 399
Db 319 CTTTTCATAGCTTGACACTTAACATCCCGTTACAGTCTCCAGTCTCACAATTACCTC 260
QY 400 TACGAGACACCGAAGTTACATCGAGTACGACCCCATATAGTGCCATCGTAGTGGCCCC 459
Db 259 GGCACATGCTCGAAGTTGCAATTTGGTTGACCCCAAAATCGAGCCCTGCTGCTCTG 200
QY 460 TAGGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTCGGGCGACCGCTATCGGT 519
Db 199 GGTTCACATTAAAGTCTCAAGATTGGCTGAGTCGAGCGCGCTGCCTCCACC--TGGAGA 142
QY 520 CGATGCCGCCCAAAAGATGTATGGACAGTTGTTTGGCGGTACTCTGATAGTGAAGCAATA 579
Db 141 GCGCCGCGGCCAGACTGTGTAGTGCATTTTGTTCAC--AATGTCAAAAAGTGGCAGCATGA 84
QY 580 GTGAAAGTCACAAA 593
Db 83 GTACAGCTACAAA 70

RESULT 15
US-08-455-244-4/c
Sequence 4, Application US/08455244
Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19895/Pl/COC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-244-4

Query Match 9.1%; Score 144.8; DB 1; Length 900;
Best Local Similarity 60.5%; Pred. No. 6.2e-27;
Matches 335; Conservative 0; Mismatches 197; Indels 22; Gaps 5;

Qy	46	GGTATCTTTGTTTGA	AAATTTGGA	AAAGACG	TAGGACACAT	-----GGACCTTGGG	99
Db	607	GGCACTTTTCTTAA	AAATCTCGA	CAATCTAG	TAGGCCCA	CATGATCCAGGCCCATTTG	548
Qy	100	TGCAACAATATTG	TGTCTCTCCAA	ATGNGTACA	AGGATTGT	TACATCTCCGGGTACTT	159
Db	547	TACAACAATATT	CAITGGTTTT	TATCACAG	TACATGGGT	TGTATACATCCACCTTGTGTTT	488
Qy	160	TAAGCTGACTAG	GACATTCAC	CAATTTAT	TATTTGCG	TGCAATTTGTTGTCATTTC	219
Db	487	TCAACTGTGCT	GGGCATTT	CGTTAAT	AGGTGCTG	TCATCTGAGATTACGACAT	432
Qy	220	CTCCACTTGG	ATTAGT	CGGGGCA	AAAGTCA	TATTAATCCATCAACTTAAAGAAA	279
Db	431	-----CCT	CAATTTGG	TCGAT	TTCCAT	TGGGATGTTAAATCCATCAACAAGAGAGA	377
Qy	280	TGTCCAGAAA	TTCTAAG	TTGTTG	AACTGCT	CGAGCGTACTCGGCTAGGTGTTTGGTG	339
Db	376	TGTCGACAAA	AGTC---	CTGAT	TGGGTTG	ATTAAAGTCAAAATTCAGCTAAAGTGTTAGGTG	320
Qy	340	GTTTTGCC	CCACCGGT	GCAC	TGCAG	GACACCAATCACCAGTCAATGCACGAACTTC	399
Db	319	CTTTTCA	TAGCCTT	GCACAT	CTTAAC	TCCGTTACAGTCTCCAGTCTCACAATTACCTC	260
Qy	400	TACCAGC	ACACCGAA	AGTTAC	ATCCAG	TACAGACCCCATATAGTGCCTAGTGTGCCCC	459
Db	259	GGCCACT	GGCCAT	CGAA	TTGCA	ATTGGTTTCGACCCCAATTCGAGCCTGGA	200
Qy	460	TAGGCGC	ATCAATG	ACCCCA	CAATTT	GGCCTCGATCGAGAGCTGGGCGACCGCCTATCGGGT	519
Db	199	GGTTCA	ATTAA	TGCTCC	AGATT	TGGCCTGAGTGGCGCGCCTGCTCCACC--TGAGA	142
Qy	520	CGATG	CGCCCA	AAACG	ATGTAT	GGACAGTTGTTTGGCGGTACTCTCGATAGTACAGCATAA	579
Db	141	GGCGG	CGCCCA	CAGC	ATG	TAGTGTAGTGTGTTTGTGAC--AATGTCAAAAGTGGCAGCATGA	84
Qy	580	GTGAA	AGTCA	CAAA	593		
Db	83	GTAA	CAGCTA	CAAA	70		

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 702.729 Seconds
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Perfect score: 1598
Sequence: 1 gtaatacagctacactatagg.....tggtgaagttggtgtttc 1598

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA.*

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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1334.4	83.5	1546	14	US-10-051-307-3
4	291.2	18.2	510	16	US-10-341-961A-371
5	186.8	11.7	735	9	US-09-938-842A-2118
6	186.8	11.7	735	11	US-09-938-842A-2118
7	186.8	11.7	950	9	US-09-770-445-334
8	168.8	10.6	875	12	US-10-636-396-4
9	168.8	10.6	875	17	US-10-636-026-4
10	161.2	10.1	909	13	US-10-424-599-103619
11	158.4	9.9	1956	13	US-10-424-599-36321
12	137.2	8.6	1173	13	US-10-424-599-7736
13	136.8	8.6	717	15	US-10-259-165-389
14	136.8	8.6	720	15	US-10-259-165-41

C 15	134.6	8.4	1006	17	US-10-437-963-86607	Sequence 86607, A
C 16	129	8.1	901	13	US-10-424-599-7737	Sequence 7737, Ap
C 17	119.4	7.5	911	13	US-10-425-114-27634	Sequence 27634, A
C 18	118.6	7.4	696	15	US-10-259-165-353	Sequence 353, App
C 19	118.6	7.4	699	15	US-10-259-165-109	Sequence 109, App
C 20	118.6	7.4	1052	17	US-10-437-963-89569	Sequence 89569, A
C 21	115.8	7.2	1020	15	US-10-259-165-371	Sequence 571, App
C 22	115.8	7.2	1020	16	US-10-260-238-3136	Sequence 3136, Ap
C 23	113.2	7.1	879	16	US-10-260-238-49	Sequence 49, Appl
C 24	109.4	6.8	805	16	US-10-260-238-4061	Sequence 4061, Ap
C 25	108.2	6.8	922	16	US-10-260-238-4067	Sequence 4067, Ap
C 26	105.6	6.6	808	9	US-09-966-881-46	Sequence 46, Appl
C 27	101.6	6.4	633	15	US-10-259-165-532	Sequence 532, App
C 28	101.6	6.4	633	15	US-10-260-238-5182	Sequence 5182, Ap
C 29	99.8	6.2	3630	17	US-10-437-963-16245	Sequence 16245, A
C 30	97	6.1	1950	17	US-10-437-963-59877	Sequence 59877, A
C 31	94.2	5.9	343	9	US-09-770-791-806	Sequence 806, App
C 32	90.8	5.7	869	17	US-10-437-963-15621	Sequence 15621, A
C 33	90.6	5.7	621	15	US-10-175-389-9	Sequence 9, Appl
C 34	89.2	5.6	621	15	US-10-175-389-1	Sequence 1, Appl
C 35	85.6	5.4	728	16	US-10-260-238-3135	Sequence 3135, Ap
C 36	84.6	5.3	1928	13	US-10-425-114-24457	Sequence 24457, A
C 37	75.8	4.7	695	15	US-10-259-165-630	Sequence 630, App
C 38	75.2	4.7	973	17	US-10-437-963-16928	Sequence 16928, A
C 39	74.4	4.7	826	13	US-10-425-114-23076	Sequence 23076, A
C 40	73.2	4.6	730	13	US-10-425-114-25389	Sequence 25389, A
C 41	70.2	4.4	935	17	US-10-437-963-82256	Sequence 82256, A
C 42	69.4	4.3	777	15	US-10-259-165-229	Sequence 229, App
C 43	68.8	4.3	529	14	US-10-051-307-6	Sequence 6, Appl
C 44	67.8	4.2	891	17	US-10-437-963-49328	Sequence 49328, A
C 45	66.4	4.2	904	13	US-10-425-114-28239	Sequence 28239, A

ALIGNMENTS

RESULT 1
US-10-051-307-2
; Sequence 2, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1598
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-2

Query Match	100.0%	Score	1598	DB 14	Length	1598
Best Local Similarity	100.0%	Pred. No	0			
Matches	1598	Conservative	0	Mismatches	0	Gaps
Qy	1	GTAATAGACTCACTATAGGACACGCGTGTGCGACGCCCGGGTGGTATCTTTGTTGA	60			
Db	1	GTAATAGACTCACTATAGGACACGCGTGTGCGACGCCCGGGTGGTATCTTTGTTGA	60			
Qy	61	AAAAATGGAAAAAGTAGGACACATGCGTGGTGCACATATTTGTGCTC	120			
Db	61	AAAAATGGAAAAAGTAGGACACATGCGTGGTGCACATATTTGTGCTC	120			
Qy	121	CAATGTGGTACAAGGATTGTTACATCTCCGGGTACTTTAAAGCTGACTAGGACATTCAC	180			
Db	121	CAATGTGGTACAAGGATTGTTACATCTCCGGGTACTTTAAAGCTGACTAGGACATTCAC	180			

Db	421	CAATGACCCACGTTTGGCCCTCGATCGAGACGTCGGCCACCGCTATCGGGGTCGATGCTG	480
QY	528	CCCAACGATGTATGGACAGTTGTTGGCCGGTACCTCGATAGTGCACAGCAATAAGTGCAAAGT	587
Db	481	CCAGACGGTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAGTGCAAAGT	538
QY	588	CACAAAGCCAGAGGGGAGAAACCAAGAGATCTCAAGTAGCCCATGTTTGGTTGAAAT	647
Db	539	CACAAAGCAGAGGGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGGTTGAAAT	598
QY	648	TTATATGTGGCAAAATTAATTTTGGTACTTTATATATAGGGATATGGGGCTTTTGGCAC	707
Db	599	TTATATGTGGCAAAATTAATTTTGGTACTTTATATATAGGGATATGGGGCTTTTGGCAC	658
QY	708	TACGGATATTAATCGTATTTATATAACAATCATCTTTGACTTAATTTATAACGAAATAT	767
Db	659	TATGGATATTAATCGTATTTATATAACAATCATCTTTGACTTAATTTATAACAATTAAT	718
QY	768	ATTACAATATGATTTGGTAAACGTTGAGTGGAAATGCTATAGAGCGCGCTTAATTAAT	827
Db	719	ATTACAATATGATTTGGTAAACGTTGAGTGGCAAAATGCTATAGAGCGCGCTTAATTAAT	778
QY	828	AATTAATTTATGAATATAGCCCTATAGTTACAAGTTAACTTTATTTGGTGATAACTTTGAC	887
Db	779	AATTAATTTATGAATATAGACTATAGTTACAAGTGAACTTTATTTGGTGATAACTTTGAC	838
QY	888	ATATAAATCTGTAAACGTGACGGATTTTTCTTAAACTAAATATTTAAAGACGAGCTAAT	947
Db	839	ATATAAATCTGTATCGTGGACGGAACCTTTCTTAAACTAAATATTTAAAGACGAGCTAAT	898
QY	948	TTCAATTTTTCGTGGCCAAAGTCTCTTGCACTACTTACTATGCCATTTTTTACTTTTAT	1007
Db	899	TTAATATTTTTCGTGGCCAAAGTCTCTTGCACTACTTACTATGCCATTTTTTACTTTTAT	958
QY	1008	CGTCTAGCCCTCTAGTGCACGTTTGACATATAAAATCATAAAAATTTGAAAGTAAAAA	1067
Db	959	CGTCTAGCCCTCTAGTGCACGTTTGACATATAAAATCATAAAAATTTGAAAGTAAAAA	1018
QY	1068	TTAGTTTTTTTTTTCATTTACTCGTATGATCATTTGTTTAGATCAATCTGGAATATAC	1127
Db	1019	TTAG--TTTTTTTTTCATTTACTCGTATGGAATCATTTGTTTAGATCAATCTGGAATATAC	1075
QY	1128	AAACCATCTGATTTTAAATCACAACCAATCTGCCCTAATGGGGAAGTCTAT--GTGATTC	1186
Db	1076	AAATCATCTGATTTTAAATCATAAATACTATCTGATGAGGAAACGCTATGCTGATTC	1135
QY	1187	GTGCAAGTGTTCGA--TTATCTTTAGTCTAGATGGAGTCACACCTTTTAGTGCAAATAT	1245
Db	1136	GTGCAAGTGTTCGATTTATCTTAAGTCTGGAATGGAGTCACACCTTTTAGTGCAAATAT	1195
QY	1246	CTATTTAAAGAACCCCTTATGATGCAAAATATCTATTTAAAGAACCCCTATTCATCTTTA	1305
Db	1196	CTATTTAAAGAACCCCTTATGATGCAAAAGTCAATAA--TATTTAAATCATCTTTA	1253
QY	1306	TTTATTTTTTACGATCGGAGATGATATATTTACTTAATTTAAATTAATTTGGGAGGAATTG	1365
Db	1254	TTTATTTTTTACGATCGGAGATGATATATTTACTTAATTTAAATTAATTTGGGAGGAATTG	1313
QY	1366	ATCGACAAGCCATCAAGCTTATCGTGCATCCATTTAGGATAACGTTAGTATGCGCTGTTT	1425
Db	1314	ATCGACAAGTCATCAAGCTTATCGTGCATCCATTTAGGATAACGTTAGTATGCGCTGTTT	1373
QY	1426	TTAGAGAAACAAGTGGATCATGATCAATTTAGGTTTAAATAATATCTCTCTATAATACCTGT	1485
Db	1374	TTAGAGAAACAAGTGGATCATGATTAATTTAGTTTTTCCCTATCTCTCTATAATATCTAT	1433
QY	1486	CTATCCCTCTTAAACCAATPACATCTAACAACAATAATAAATTTAGATTTCCCTTAAGA	1545
Db	1434	ATATACCTCTAAACTTAATGATCTTAACAACAATTAATACTTAGATTTCTTTTAAGA	1493
QY	1546	AATTCAGAAATTAATTTGGAGCAAAATAGTCTTAATGGTGAAGTTGGTTGCTTTC	1598

Db 1494 AATTGCAGAATTAAATGGAGGCAATAAGTCTATGGTGAAGTTGGTTGCTTTC 1546

RESULT 4

```

US-10-341-961A-371/c
; Sequence 371, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Crasta, Oswald
; APPLICANT: Swirsky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGEN
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
; FILE REFERENCE: BTI-67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 371
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-371

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Query Match	18.2%	Score 291.2	DB 15	Length 510
Best Local Similarity	78.1%	Prod. No. 1.7e-54		
Matches 350	Conservative 0	Mismatches 98	Indels 0	Gaps 0
QY	49	ATCTTTCTTTGAAAAAATGGAAAAAGACGTAGGACCACTAGGACCTTGGGTGCACAAAT	108	
Ddb	448	ATCTTTCTTTGAAAAATCTTGACATTCAGTAGGACCACATGGACCGTGATACACAAAT	389	
QY	109	ATTGTTGTCCTCCAAATGTGTCACAGGATTGTTACATCTCCGGGTACTTTTAAGCTCAC	168	
Ddb	388	ATTGTTGTCCTCCGAATGTTGTACAGGGTGTGTTACATCTCCAGGTACCCCTAAGTGAAC	329	
QY	169	TAGGACATTCACCATTTATATTGGCGTGCAATTGAATGTGTGGCATTTCCCTCCACTTG	228	
Ddb	328	CAGGGCAATTCACCGTTTATATTGGCTGTGCATTTGAATTTGGATGACATTTCCAGGGCCAG	269	
QY	229	GATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCCAGA	288	
Ddb	268	GCTTAGTTGGGCCAAAGAAGACATAGGAGTGTGAAATCCATCAATACACAGAAATATCCCAA	209	
QY	289	AATCTAAGTTGTGTGACTCGTCCAGGGGTACTCGGTAGGGTGTGTGGTGGTTGGCCCC	348	
Ddb	208	AATCTAGGTTACCAAACTGGTTCAAAGCGTATTACGTAAAGTGTGTGGTGGTTTACCCCC	149	
QY	349	ACCGGTGCATCGAGGACACACCACAATCAACCAAGTCATCGACGAACCTCTACAGCAC	408	
Ddb	148	ATCCTTTGCAATCCAGGACTCCACCACAATCACCAGTCTGGCACCAACCTCTTCCAGCAC	89	
QY	409	CACCGAAGTTTACATCCAGTACGACCCCAATATACGTGGCCATCGTAGTGCCCTTAGCGCAT	468	
Ddb	88	CATCAAGTTGCATTAATGATACGACCCCAAAATACGTGCCATTTTAGTGCAGGTGGGGCCC	29	
QY	469	CAATGACCACATTTGGGCTCGATCGAG	496	
Ddb	28	AAACACCAACTCTGACCTCTCTCGAG	1	

RESULT 5

US-09-938-842A-2118/c
; Sequence 2118, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 11.7%; Score 186.8; DB 9; Length 735;
Best Local Similarity 62.4%; Pred. No. 3.1e-31;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;
Qy 46 GGTATCTTTGTTGAAAAATTTGAAAAAGAACGTAGGACCAATG-----GACCTTGGG 99
Db 586 GGCATCTCTGCTTAAGAAATCTTGAGTACTCAGTATCGGTACATGATCCCTGACCGGTG 527
Qy 100 TGCACAAATATTTGTTCTCCAAATGTTGTTCAAGAGTATTTACATCTCCGGGTACTT 159
Db 526 TACAACAGTATGTTGCTGCTGAAATACAGTACACGGGTGTTGTCATCCACCTCGGGCTC 467
Qy 160 TAAGCTGACTAGGACATTCACATTTATTTGCGGTGCAATGTAATTTGTGGCAATTTCC 219
Db 466 TCAACAGTTTGGACATTTGCTGTTTATCTGCGGTACATAGTATCCGATGGCAGTTC- 408
Qy 220 CTCACCTTGGATTTAGTCGGGGCGAAAGTCACTAGTATGTTAAATCCATCAACTAAAGAAA 279
Db 407 -----GAACTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAAGTGA 356
Qy 280 TGTCCAGAAATCTAAGTTGTTGAATCTGCTCAAGCGTACTCGGCTAGGGTGTGTTGGTG 339
Db 355 TATCGTAGAGTCTAAGTTGTTGAATCTGCTCAAGCGTACTCGGCTAGGGTGTGTTGGTG 296
Qy 340 GTTTCGCCACCCCGGTGCACTGCGAGGACACCAACCAATCACTAGTATCGACCAACCTC 399
Db 295 GCTGTCCCGACCGAGTACATTTGGATTTGGTTCAAGCGTACTCGACCAACCTC 236
Qy 400 TACGAGCACCACCGAGTACATTTGGCTCGATCGAGACGTGCGGCACCGCTATCGGGT 459
Db 235 GACCTGAGGAGTCAAAAGTTCAATTTGGTCTTACCCCAATCCGTCGCCATTTAGTGCCG 176
Qy 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGCACCGCTATCGGGT 519
Db 175 CCGGACATCTAGCTTCCATGTTGGCAGCATCTAGACGTGCGGCACCTCC--AGGGCT 118
Qy 520 CGATCGCGCCMAAGCATTTAGGACAGTTTGTGGCGTACTCTGATAGTACAGCATAA 579
Db 117 TCGCGCAGCCCAACCGGTGTAATCACTATTGTT--TAGGATTTGGAATGTGGCGCTGTT 60
Qy 580 GTGAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
Db 59 GCGGTGGAGATGACGAAAGTCCGGAATATGAAAGTAGAGACCAAG 12

RESULT 6
US-09-938-842A-2118/c

; Sequence 2118, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 11.7%; Score 186.8; DB 11; Length 735;
Best Local Similarity 62.4%; Pred. No. 3.1e-31;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;
Qy 46 GGTATCTTTGTTGAAAAATTTGAAAAAGAACGTAGGACCAATG-----GACCTTGGG 99
Db 586 GGCATCTCTGCTTAAGAAATCTTGAGTACTCAGTATCGGTACATGATCCCTGACCGGTG 527
Qy 100 TGCACAAATATTTGTTCTCCAAATGTTGTTCAAGAGTATTTACATCTCCGGGTACTT 159
Db 526 TACAACAGTATGTTGCTGCTGAAATACAGTACACGGGTGTTGTCATCCACCTCGGGCTC 467
Qy 160 TAAGCTGACTAGGACATTCACATTTATTTGCGGTGCAATGTAATTTGTGGCAATTTCC 219
Db 466 TCAACAGTTTGGACATTTGCTGTTTATCTGCGGTACATAGTATCCGATGGCAGTTC- 408
Qy 220 CTCACCTTGGATTTAGTCGGGGCGAAAGTCACTAGTATGTTAAATCCATCAACTAAAGAAA 279
Db 407 -----GAACTAGTTGGGCTAAACTCCATAGTATGTTAAATCCATCGACAAAGTGA 356
Qy 280 TGTCCAGAAATCTAAGTTGTTGAATCTGCTCAAGCGTACTCGGCTAGGGTGTGTTGGTG 339
Db 355 TATCGTAGAGTCTAAGTTGTTGAATCTGCTCAAGCGTACTCGGCTAGGGTGTGTTGGTG 296
Qy 340 GTTTCGCCACCCCGGTGCACTGCGAGGACACCAACCAATCACTAGTATCGACCAACCTC 399
Db 295 GCTGTCCCGACCGAGTACATTTGGATTTGGTTCAAGCGTACTCGACCAACCTC 236
Qy 400 TACGAGCACCACCGAGTACATTTGGCTCGATCGAGACGTGCGGCACCGCTATCGGGT 459
Db 235 GACCTGAGGAGTCAAAAGTTCAATTTGGTCTTACCCCAATCCGTCGCCATTTAGTGCCG 176
Qy 460 TAGGCGCATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGCACCGCTATCGGGT 519
Db 175 CCGGACATCTAGCTTCCATGTTGGCAGCATCTAGACGTGCGGCACCTCC--AGGGCT 118
Qy 520 CGATCGCGCCMAAGCATTTAGGACAGTTTGTGGCGTACTCTGATAGTACAGCATAA 579
Db 117 TCGCGCAGCCCAACCGGTGTAATCACTATTGTT--TAGGATTTGGAATGTGGCGCTGTT 60
Qy 580 GTGAAGTCAAAAAGCCAGAGGAGAAACCAAAAGAGATCTCAAG 627
Db 59 GCGGTGGAGATGACGAAAGTCCGGAATATGAAAGTAGAGACCAAG 12

RESULT 7
US-09-770-445-334/c
; Sequence 334, Application US/09770445

```

; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Naja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hufban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-334

Query Match      11.7%; Score 186.8; DB 9; Length 950;
Best Local Similarity 62.4%; Pred. No. 3.6e-31;
Matches 367; Conservative 0; Mismatches 202; Indels 19; Gaps 4;

QY 46 GGTATCTTTGTTGAAATAATGGAAAGAACGTAGACACACATG-----GACCTTGGG 99
DB 594 GGCATCTCTGCTTAAAGAACTTTGAGTACTACGTATCGCTACATGATCCCTGACCGTTG 535
QY 100 TGCACATATTTGTTCCCTCAAATGTTGTAACAAGATTTTACATCTCTCCGGTACTT 159
DB 534 TACAACAGTATTGGTTGCTCTGAAATACAGTACACGGGTTTGTGATCCACCTGGGGCTC 475
QY 160 TAAGCTGACTAGACATTTACACATTTATATTTCCCGTGCATTGAATTTGTTGCAATTTCC 219
DB 474 TCAACAGTTTGACATTTGCTGTTTATGTTGCTGGGTACATAGTATCCGATGGCGTTTC 416
QY 220 CTCACCTGATTTAGTTCGGGGGAAAGTCACTGGTATATTTAAATCCATCAACTAAAGAAA 279
DB 415 -----GAACTAGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGACAGTGAGA 364
QY 280 TGTCCAGAAATCTAGTTGTTGAATCTGCTGCAAGCGTACTCGCTAGGTTGTTGGTG 339
DB 363 TATCGTAGAAGTCTAGTTGTTGAATTTGTTCAAGCGTACTCAGCCAACTGTTTGGTG 304
QY 340 GTTTGCCCCACCGGTGCACTGCGAGACACCAACCAATCACCAGTCAATGCAAGAACCTC 399
DB 303 GCTGTCCCCAGCGAGTACATTTGGAGTCCACCACTGCAGTCAACAGTTTGGCATCGGCCAC 244
QY 400 TACCAGCACCCAGAGTTTACATCCAGTACGACCCCATATAGTGGCATCTGTTAGTGGCCC 459
DB 243 GACCTGAGGAGTCAAAAGTTTACAAATTTGGTCTTACCCCAATCCGTGCCATTTTGTAGTGG 184
QY 460 TAGGGCGCATCAATGACCCACATTTGGCCCTCGATTCGAGACGTGGGACCGCCCTATCGGGT 519
DB 183 CCGCGACATCTAGCTCCATGATTTGGCCAGCATCTAGAGTTCGGGCCACTTCC--AGGGCT 126
QY 520 CGATGCCGCCAAACGATGTATGGACAGTTGTTGGGGTACTCCTGATAGTACACATAA 579

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; Sequence 4, Application US/10636396
; Publication No. US20040073971A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,396
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-4

Query Match      10.6%; Score 168.8; DB 12; Length 875;
Best Local Similarity 61.3%; Pred. No. 3.4e-27;
Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;

QY 49 ATCTTTGTTGTAATAATTTGAAAGAACGTAGACACACATGACCTTGGGTGCAACAAT 108
DB 577 ATCTGGTCTTGAATAAACCTTTGATAAATCAGTTGTCACAAATTTCCAGAGTTGCAACAAT 518
QY 109 ATTGTGTCTCCAAATGTTGTACAGGATTTGTACATCTCCGGGTACTTTAAGCTGAC 168
DB 517 ACTGATCAGTTTGTACACGGTGCNAGGTTATTGACCCGCGAGGAGCCGTAATCTAC 458
QY 169 TAGACATTCACATTTATATTTCCTGCGTGCATTAATTTGTGGCATTTTCCCTCCACTTG 228
DB 457 CAGGACACTGCGCATTTGATATCCGCACTACATGAGATACCCCGGTGCACCC-----AT 404
QY 229 GATTAGTCGGGGCAAGTTCATCGGTATATTAAATCATCACTAAGAAATGTCGCCGA 288
DB 403 TAGAATTTGGTCTTAACACCATCGGCATTTGAATTCGTCCTCAAGAGAAATGTCAAAGA 344
QY 289 AATCTAAGTTTGTGAATCTGTTCCAAAGCGTACTCGGTAGGGTGTGTTGTTGGTCC 348
DB 343 AATCAAGATTTGTTGAATCTGTTTCAAAGCGTACTCGGCAATGTTTGGGTGGGTACCAT 284
QY 349 ACCCGGTGCTACGAGACACCAACCACTCAGCATCTGACGACCTTACAGGAC 408
DB 283 AGTTTGGCATTTGAGAGACCGTTTGAATCACCCTGCTGACACCTGCTCCCTCCGAGAAC 224
QY 409 CACCGAAGTTTACATCCAGTACGACCCCATATAGTGCATTCGTAGTGCCTTAGGCGCAT 468
DB 223 CATCAAGATTTGCAATTTGTTTCGGGGCCATATACGGGCTCTCTGCTGTGCCAGTGCACGG 164
QY 469 CAATGACCCACATTTGGCTTCGATCGAGAGTGGGACCGGCTATCGGGTTCGATCCCGC 528
DB 163 TTAAAGACAGGTTTGGCTGAGTTAAGTTGTTGCGCGCCACC--AGGCACCGCACGAC 106

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Qy 529 CCAAAACGATGTATGGACAGTTGTT 552
Db 105 CCAAAACGTTGTATGGACAGTTGTT 82

RESULT 9

US-10-636-026-4/c
; Sequence 4, Application US/10636026
; Publication No. US20040111761A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guohua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,026
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-026-4

Query Match 10.6%; Score 168.8; DB 17; Length 875;
Best Local Similarity 61.3%; Pred. No. 3.4e-27;
Matches 309; Conservative 0; Mismatches 187; Indels 8; Gaps 2;

Qy 49 ATCTTTGTTTCAAAAAATTTGAAAGACGATGACACATGGACCTTGGGTGCAACAAT 108
Db 577 ATCTGCTTTGAAAACCTTGAATAATCAGTTGGTCCACAATTTCCAGAGTTGCAACAAT 518
Qy 109 ATTGTGTCCTCCAAATGTGTACAAAGATTTGTATCATCTCCGGGTACTTTAAGCTGAC 168
Db 517 ACTGATCAGTTTGTACACGGTGTCAAGGTTATTGACCCCGCAGGAGCCCGTAATCTAC 458
Qy 169 TAGGACATTCACCATTTATTTCCGTCGATTTGATTTGTGGCATTTCCCTCCACTTG 228
Db 457 CAGGACATCGCCATTGATATCCGCGATACATGAGATACCCCGGTGACCC-----AT 404
Qy 229 GATTAGTCGGGCGGAAAGTCATCGGTATATTAAATCCATCACTAAAGAAATGTCCAGAC 288
Db 403 TAGAATCGGTCTAAACACCATCGGCACATTGAATCCGTCACAAAGAGAAATGTCAAAGA 344
Qy 289 AATCTAAGTTGTGAACCTGGTCCAAAGGCTACTCGGCTAGGGTGTTTGGTGGTTGCCCC 348
Db 343 AATCAAGATTTGTGAACCTGGTTCAAAGGCTACTCGGCCAATGTGTGGTGGGTGACCAT 284
Qy 349 ACCCGGTGCACTGACGAGGACACCAACCAATCACCAGTATGTCAGCAACCTCTACAGCAC 408
Db 283 AGTTTGGCAATTGGAGAGACCGTTGCAATCACCGGTCTGACACTGCTCGCCAGAAC 224
Qy 409 CACCGAAGTTACATCCAGTACGACCCCATATACGTCGCATCGTAGTGCCTCCATGCGGCAT 468
Db 223 CATCAAGTTGCAATTTGGTTCGGGGCCATATACGGGCTCTGCTGTGCGAGCTGCGACGG 164
Qy 469 CAATGACCCACATTTGGCTCGATCGAGNCTCGGGCAGCCGCTATCGGGTCGATGCGGC 528
Db 163 TTAAGAACAAGTTTGGCTGAGTTAAGTTGTGCGCCGCCACCC--AGCACCGCACACAGC 106
Qy 529 CCAAAACGATGTATGGACAGTTGTT 552
Db 105 CCAAAACGTTGTATGGACAGTTGTT 82

RESULT 10

US-10-424-599-103619/c
; Sequence 103619, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103619
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
US-10-424-599-103619

Query Match 10.1%; Score 161.2; DB 13; Length 909;
Best Local Similarity 61.1%; Pred. No. 1.7e-25;
Matches 314; Conservative 0; Mismatches 193; Indels 7; Gaps 3;

Qy 46 GGTATCTTTGTTGAAAAAATTTGAAAAGACGATGAGGACACATGGACCTTGGGTGCAAC 105
Db 631 GGCACCTTTGCTTGAAGAATCTGGAATAATCATGTGGGCCACAGCTACCGGAATTGCAAC 572
Qy 106 AATATTGTTGCTCTCCAAATGTGTACAAGGATTTTACATCTCCGGGTACTTTAAGCT 165
Db 571 AGTACTGTTGGTGTTCGAAGACAGTCAAGGGTGTGTGCAACCTCTTGGAGCTTTAGCT 512
Qy 166 GACTAGCAATTCACCAATTTATTTGCGGTGATGATGATGATGATGATGATGATGATGAT 225
Db 511 CACTAGGCGACTGCTCGGTTAATGTCGCAAGTGA---GCTTATGCCACGTTGTCATCCAT 455
Qy 226 TTGGATTAGTCGGGCGGAAAGTATCGGTATATTAAATCCATCACTAAAGAAATGTCCTC 285
Db 454 TCG---AGTTGGACTTAAAGTCCATGGGCACGTTAAACCCGTCGACGAGGAGATGTGA 398
Qy 286 AGAAATCTAAGTTGTTGAACTGCTGTCAGGCGGTACTCGGCTAGGGTGTGTTGGTGTTC 345
Db 397 AGAAGTCCAAATTTGTAACCCGTTTCAGGCGGTATTTCAGCCAGGGTGTGGGAGGCGCAC 338
Qy 346 CCACCCGGTGCATCGAGACACCAACCAATCACCAGTATGACAGTATGACAGTATGACAG 405
Db 337 CGTAAGCTTTGCACTGAGGACACCCCGCAGTCACCGGTCTGGCATCCACCGCGGCGCG 278
Qy 406 CACCACCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGGCG 465
Db 277 AACGTCGAAGTTGACGCGGTTCGGGCCCAACAGCGGGCCCTTTTCTTCTGCGAGGCA 218
Qy 466 CATCAATGACCCACATTTGGCTCGATCGAGAGCTCGGGACCGCCCTATCGGGTCTGATG 524
Db 217 CGTCCACGAGACCATGATGCTGCGCGGTTTAAATTGACGCGCACCGCCCAACAGGACAGC 158
Qy 525 CCGCCCAACGATGATGGACAGTTGTTGGCGT 558
Db 157 CAGCCCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 124

RESULT 11

US-10-424-599-36321/c
; Sequence 36321, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K


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; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 389
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-389

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Query Match      8.6%; Score 136.8; DB 15; Length 717;
Best Local Similarity 58.8%; Pred. No. 3.9e-20;
Matches 274; Conservative 0; Mismatches 187; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTGTACATCTCTCCGGGTAC 157
DB 541 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTGTACATCTCTCCGGGTAC 482
QY 158 TTTAAGCTGACTAGGACATTCACCAATTTATTTGCGGTGCAATTTGATTTGTTG 213
DB 481 CCTAGCTGCTCGGGGACTGCGCCGCGCACGTCGCGCCGCGCCGCGCCGCTTGGC 422
QY 214 ATTTCCCTCCACTTGGATTAGTCGGGGGCGAAAGTCATCGGTATATTAATCAACTA 273
DB 421 GCACCCGCGCGCTGCGCGGGGAGGAGTCCATGGGCACTGGAATCCGTCGATGA 362
QY 274 AAGAAATCTCCAGAAATCTAAGTTGTTGAATCTGTCAGAGCGTACTCGCTAGGTTGT 333
DB 361 GGGAGATGTCGAAGAAGTCGAGGTTGCTGAATCTGTTGAGCGCACTTCCGCCAGCGTGT 302
QY 334 TTGCTGTTTGGCCCAACCGGTGCACTGCAGGACACACCAATCAACAGTCATGACAG 393
DB 301 TGGCGGCTGCGCGTACGCGCGCACGCGCACGCGCGCGCGCGCGCTTGGCAC 242
QY 394 AACCTTACAGCAGCACCGAAGTTATCATCAGTAGACACCCATATAGTGCCATCGTAG 453
DB 241 GCCGTTGCCGCTGCGCGTGAAGTCGAGCGCGTGCAGCGCGCACACGCGCGCGCGTGC 182
QY 454 TGCCCTAGGCGCATCAATGACCCACATTTGCGCTCGATCGAGACGTCGCGCACCGCTA 513
DB 181 TGCGCGCGCGCACGTCGATCACCACCTGCTGCGCGCGGTCCAGCTGCTGCGCGCGCG 122
QY 514 TCGGCTCG-ATGCGCGCGCAACGATGTATGACAGTTGTTGCGCGT 558
DB 121 ACGGCACGCGTGC CGCGCGCACACGCGTGTATCGGCACTTGTGTTGAT 76

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RESULT 14
US-10-259-165-41/c
; Sequence 41, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hui-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

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; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 41
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-41

Query Match      8.6%; Score 136.8; DB 15; Length 720;
Best Local Similarity 58.8%; Pred. No. 3.9e-20;
Matches 274; Conservative 0; Mismatches 187; Indels 5; Gaps 2;

QY 98 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTGTACATCTCTCCGGGTAC 157
DB 541 GGTGCAACAATATTTGTTCTCCAAATGTGGTACAGGATTTGTACATCTCTCCGGGTAC 482
QY 158 TTTAAGCTGACTAGGACATTCACCAATTTATTTGCGGTGCAATTTGATTTGTTG 213
DB 481 CCTAGCTGCTCGGGGACTGCGCCGCGCACGTCGCGCCGCGCGCCGCTTGGC 422
QY 214 ATTTCCCTCCACTTGGATTAGTCGGGGGCGAAAGTCATCGGTATATTAATCAACTA 273
DB 421 GCACCCGCGCGCTGCGCGGGGAGGAGTCCATGGGCACTGGAATCCGTCGATGA 362
QY 274 AAGAAATCTCCAGAAATCTAAGTTGTTGAATCTGTCAGAGCGTACTCGCTAGGTTGT 333
DB 361 GGGAGATGTCGAAGAAGTCGAGGTTGCTGAATCTGTTGAGCGCACTTCCGCCAGCGTGT 302
QY 334 TTGCTGTTTGGCCCAACCGGTGCACTGCAGGACACACCAATCAACAGTCATGACAG 393
DB 301 TGGCGGCTGCGCGTACGCGCGCACGCGCACGCGCGCGCGCGCTTGGCAC 242
QY 394 AACCTTACAGCAGCACCGAAGTTATCATCAGTAGACACCCATATAGTGCCATCGTAG 453
DB 241 GCCGTTGCCGCTGCGCGTGAAGTCGAGCGCGTGCAGCGCGCACACGCGCGCGCGTGC 182
QY 454 TGCCCTAGGCGCATCAATGACCCACATTTGCGCTCGATCGAGACGTCGCGCACCGCTA 513
DB 181 TGCGCGCGCGCACGTCGATCACCACCTGCTGCGCGCGGTCCAGCTGCTGCGCGCGCG 122
QY 514 TCGGCTCG-ATGCGCGCGCAACGATGTATGACAGTTGTTGCGCGT 558
DB 121 ACGGCACGCGTGC CGCGCGCACACGCGTGTATCGGCACTTGTGTTGAT 76

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RESULT 15
US-10-437-963-86607/c
; Sequence 86607, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 05:06:40 ; Search time 3757.1 Seconds
(without alignments)
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Perfect score: 1598
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estm.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_est3.*
- 12: gb_est4.*
- 13: gb_est5.*
- 14: gb_est6.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	474.6	29.7	899	14	CK252883
c 2	474.6	29.7	1004	14	CK248798
c 3	471.4	29.5	988	14	CK246326
c 4	469.6	29.4	888	14	CK278032

c 5	469	29.3	853	14	CK271811	CK271811 EST17889
c 6	468.6	29.3	899	14	CK252271	CK252271 EST173508
c 7	465.2	29.1	739	12	BI176339	BI176339 EST521139
c 8	456.6	28.6	649	9	AW039873	AW039873 EST282346
c 9	455.2	28.5	583	12	BI432833	BI432833 EST535594
c 10	451.6	28.3	639	12	BI430890	BI430890 EST463582
c 11	449.6	28.1	667	12	BI922472	BI922472 EST542376
c 12	449	28.1	622	10	BF053678	BF053678 EST438908
c 13	447.2	28.0	585	9	AW031249	AW031249 EST274624
c 14	440.8	27.6	583	9	AW032915	AW032915 EST276474
c 15	439.2	27.5	923	14	CK273930	CK273930 EST720008
c 16	439	27.5	649	10	AW222204	AW222204 EST299015
c 17	439	27.5	652	12	BI921170	BI921170 EST541073
c 18	439	27.5	669	12	BI921735	BI921735 EST541638
c 19	439	27.5	782	12	BM410787	BM410787 EST585114
c 20	438.8	27.5	598	14	CA514039	CA514039 KS09015D0
c 21	437.8	27.4	651	10	AW218785	AW218785 EST301265
c 22	436.8	27.3	777	12	BM407898	BM407898 EST582255
c 23	435.8	27.3	586	9	AW033588	AW033588 EST27159
c 24	431.8	27.0	944	14	CK271145	CK271145 EST717223
c 25	430	26.9	657	10	AW223507	AW223507 EST300318
c 26	427.4	26.7	936	14	CK277819	CK277819 EST723897
c 27	426.8	26.7	575	12	BI421330	BI421330 EST531996
c 28	426.6	26.7	629	10	BE432710	BE432710 EST399239
c 29	425.8	26.6	574	10	AW441774	AW441774 EST311170
c 30	425.8	26.6	776	12	BI423560	BI423560 EST469306
c 31	425.6	26.6	916	14	CK279273	CK279273 EST725351
c 32	425.6	26.6	638	12	BI434454	BI434454 EST537215
c 33	425.6	26.6	757	12	BI434095	BI434095 EST536856
c 34	425	26.6	604	12	BI423179	BI423179 EST533845
c 35	425	26.6	637	12	BI921311	BI921311 EST541214
c 36	425	26.6	719	12	BI422260	BI422260 EST532926
c 37	425	26.6	720	12	BI921826	BI921826 EST541729
c 38	425	26.6	807	12	BI421946	BI421946 EST532612
c 39	424.2	26.5	574	10	AW223623	AW223623 EST300434
c 40	424	26.5	626	9	AW033829	AW033829 EST277400
c 41	423	26.5	682	10	AW223970	AW223970 EST300781
c 42	423	26.5	710	9	AW035171	AW035171 EST280433
c 43	422.8	26.5	573	9	AW032317	AW032317 EST275771
c 44	422.4	26.4	660	12	BM403979	BM403979 EST578306
c 45	421.6	26.4	626	12	BI421167	BI421167 EST531833

ALIGNMENTS

RESULT 1
CK252883/c 899 bp mRNA linear EST 12-DEC-2003
LOCUS
DEFINITION
EST736520 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POC086 5' end, mRNA sequence.
ACCESSION
CK252883
VERSION
CK252883.1 GI:39807285
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 899)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
AUTHORS
Generation of ESTs from potato callus tissue
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: Arr TAG GTG ACA CTA TAG.
Location/Qualifiers
1. .899
/organism="Solanum tuberosum"
/mol_type="mRNA"

Db	12	ACTATATTTTT 2	
Db	241	CACCATCAAAAGTTGCAATTAGTAGCACCACCATATACGTGCCTTCTTAGTGCCTCCCTCGGCG 182	
Qy	466	CATCAATGACCCACATTTGGCCCTCGATCGAGACGTCGGCACCCTATC-GGTCGATG 524	
Db	181	CATTGATAACCCATGTCTGGCTCGATCGAGACGTCGGCACCCTATGTCGGGTGATG 122	
Qy	525	CCGCCAAACGATGTATGACAGTCTTGTGGCGTACTCGATAGTACAGTACAGTAAAGTGA 584	
Db	121	CGCCCCACACGGGTGTATGACAGTATTG-CGTACTCGATAGTGGCAGCATAGTGA 64	
Qy	585	AGTCACAAAGCCAGAGGAGGAGAAACCAAGAGATCTCAAGTAGCCCATGTTTGTGA 644	
Db	63	AGTCACAAAGCAAGGAGGAGGAGAAACCAAGAGATCTCAAGTAGCCCATGTTTGTGA 4	
Qy	645	AAT 647	
Db	3	ACT 1	
RESULT 4			
LOCUS	CK278032/c		
DEFINITION	EST724110 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE351 5' end, mRNA sequence.		
ACCESSION	CK278032		
VERSION	CK278032.1	GI:39835010	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	1 (bases 1 to 888)		
TITLE	Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.		
JOURNAL	Generation of ESTs from abiotic stressed potato tissue		
COMMENT	Unpublished (2003)		
	Other ESTs: EST724111		
	Contact: Robin Buell		
	The Institute for Genomic Research		
	9712 Medical Center Dr, Rockville, MD 20850, USA		
	Email: potato-array@tigr.org		
	Clones can be requested from TIGR via potato@tigr.org		
	Seq primer: ANT TAG GTG ACA CTA TAG.		
FEATURES	Location/Qualifiers		
source	1..888		
	/organism="Solanum tuberosum"		
	/mol_type="mRNA"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="POAE351"		
	/tissue_type="abiotic stress treated leaf and root tissue"		
	/lab_host="DH10B-TonA"		
	/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d, 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Brought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d, 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr,		
Query Match	29.5%;	Score 471.4;	DB 14; Length 988;
Best local Similarity	88.6%;	Pred. No. 6.9e-86;	
Matches 534;	Conservative 0;	Mismatches 56;	Indels 3; Gaps 2;
Qy	46	GGTATCTTTGTTGAAAAAATTGGAAGAAGACGTAGGACCAATGACATGACCTTGGGTGCAAC 105	
Db	601	GGCATCTTTGTTGAAAAAATTGACAAATCAGTAGGACCAATGACCTTGGGTGCAAC 542	
Qy	106	AATATTGTTGCTCCCAATGTTGACAGGATTTTACATCTCCGGGTACTTTAAGCT 165	
Db	541	AATATTGTTGCTCCGAACTGTTGACAGGATTTTACATCTCCAGGTACCTTAAGT 482	
Qy	166	GACTAGGACATTCACATTTATTTGCGGTGCAATGAAATTTGTGTGCAATTCCTCCAC 225	
Db	481	AACAGGACATTCACATTTATTTAGCGGTGCAATGAAATTTGTGTGCAATTCCTCCAC 422	
Qy	226	TTGATTTAGTGGGGCGAAGTCATGCGTATTTAAATTCATCACTAAAGAAATGCCC 285	
Db	421	TAGGATTTGTTGGGCGAAGTCATCGGAATTTAAATTCATCACTAAAGAAATGCCC 362	
Qy	286	AGAAATCTAAGTTGTTGAACCTGTTCCAGGGGTACTCGGTAGGCTTTGTTGGTTTC 345	
Db	361	AGAAATCTAAGTTGTTGAACCTGTTCCAGGGGTACTCGGTAGGCTTTGTTGGTTTC 302	
Qy	346	CCACCCGGTGCATCGAGGACACCAACCAATCACCAGTCAATGACGAACTTACAG 405	
Db	301	CCACCCGGTGCATCGAGGACACCAACCAATCACCAGTCAATGACGAACTTACAG 242	
Qy	406	CACACCGGAAGTTACATCCAGTAGACCCCATATACGTGCATCGTAGTCCCTTAGCG 455	

12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

```

ORIGIN
Query Match      29.4%; Score 469.6; DB 14; Length 888;
Best Local Similarity 88.8%; Pred. No. 1.7e-87;
Matches 531; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAGAGACGTAGGACACATGGACCTTGGTGGCAAC 105
DB 597 GGCATCTTTGTTGAAAAAATCTGACAAATCAGTAGGACACATGGACCTTGGTGGCAAC 538
QY 106 AATATTGTTGCTCCCAAAATGTGTACAAAGATTGTTACATCTCCCGGTTACTTTAAGCT 165
DB 537 AATATTGTTGCTCCCAAAATGTGTACAAAGATTGTTACATCTCCCGGTTACTTTAAGCT 478
QY 166 GACTAGGACATTCACCAATTTATTTGCGTGCATTTGAATTTGTTGTCATTTCCCTCCAC 225
DB 477 AACAGGACATTCACCAATTTATTTAGCCGTGCAATGATTTGCGTGCATTTCCCTCCAC 418
QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCCACTCAAAAGAAATGTCCC 285
DB 417 TAGGATTGTTGGGGCGAAAGTCATCGGAATTTAAATCCCACTCAAAAGAAATGTCCC 358
QY 286 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGGTACTCGGCTAGGGTGTTCGTTGGTTGC 345
DB 357 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGGTACTCGGCTAGGGTGTTCGTTGGTTGC 298
QY 346 CCCACCCCGTGCACATGTCAGGACACCCACCAATCACCAATCACCAATCTGCGATGAACTTACCAG 405
DB 297 CCCACCCCGTGCACATGTCAGGACACCCACCAATCACCAATCACCAATCTGCGATGAACTTACCAG 238
QY 406 CACCAACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTTAGCGC 465
DB 237 CACCAATCAAGTTGCAATTTAGTACGACCCCATATACGTGCCATCTTAGTGCCTCCGCGC 178
QY 466 CATCAATGACCCACATTTTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGTTCGATG 524
DB 177 CATGATACCATGCTCTGGCTCGATCGAGACGTGCGGGCACCCGCTATCGGGTTCGATG 118
QY 525 CCGCCCAACGATGTATGACAGTTGTTGGCGTACCTCGATGATGACACATAGTGAA 584
DB 117 CCGCCCAACGATGTATGACAGTTGTTG--CGTACCTCGATGATGTCGACATAGTGTA 60
QY 585 AGTCACAAAGCCAGAGGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTGT 642
DB 59 AGTCACAAAGCCAGAGGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTGT 2

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RESULT 5
CK271811/c
LOCUS
DEFINITION
EST17889 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAD143 5' end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

1 (Bases 1 to 853)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST17890

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source

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Location/Qualifiers
1..853
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/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAD143"
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/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d.
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

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ORIGIN

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Query Match      29.3%; Score 469; DB 14; Length 853;
Best Local Similarity 88.6%; Pred. No. 2.3e-87;
Matches 531; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTGAAAAAATTTGAAAGAGACGTAGGACACATGGACCTTGGGTGCAAC 105
DB 597 GGCATCTTTGTTGAAAAAATCTAGCAAAATCAGTAGGACACATGGACCTTGGGTGCAAC 538
QY 106 AATATTGTTGCTCCCAAAATGTGTACAAAGATTGTTACATCTCCCGGTTACTTTAAGCT 165
DB 537 AATATTGTTGCTCCCAAAATGTGTACAAAGATTGTTACATCTCCCGGTTACTTTAAGCT 478
QY 166 GACTAGGACATTCACCAATTTATTTGCGTGCATTTGAATTTGTTGCGATTTCCCTCCAC 225
DB 477 AACAGGACATTCACCAATTTATTTAGCCGTGCAATGATTTGCGTGCATTTCCCTCCAC 418
QY 226 TTGGATTAGTCGGGGCGAAAGTCATCGGTATTTAAATCCCACTCAAAAGAAATGTCCC 285
DB 417 TAGGATTGTTGGGGCGAAAGTCATCGGAATTTAAATCCCACTCAAAAGAAATGTCCC 358
QY 286 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGGTACTCGGCTAGGGTGTTCGTTGGTTGC 345
DB 357 AGAATCTAAGTTGTTGAACCTGGTCCAAAGGGTACTCGGCTAGGGTGTTCGTTGGTTGC 298
QY 346 CCCACCCCGTGCACATGTCAGGACACCCACCAATCACCAATCACCAATCTGCGATGAACTTACCAG 405
DB 297 CCCACCCCGTGCACATGTCAGGACACCCACCAATCACCAATCACCAATCTGCGATGAACTTACCAG 238
QY 406 CACCAACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTTAGCGC 465
DB 237 CACCAATCAAGTTGCAATTTAGTACGACCCCATATACGTGCCATCTTAGTGCCTCCGCGC 178
QY 466 CATCAATGACCCACATTTTGGCTCGATCGAGACGTGCGGGCACCCGCTATC-GGGTTCGATG 524
DB 177 CATGATACCATGCTCTGGCTCGATCGAGACGTGCGGGCACCCGCTATCGGGTTCGATG 118
QY 525 CCGCCCAACGATGTATGACAGTTGTTGGCGTACCTCGATGATGACACATAGTGAA 584

```

Db 117 CGCCCCACACGGTGTATGACAGTTATTG--CGTACCTCGATAGTGGCAGCATAAAGTGA 60

Qy 585 AGTCACAAAAGCGCAGAGGAGAAACCAAGAGAGATCTCAAGTAGCCCATGTTTGTG 643

Db 59 AGTCACAAAAGCGCAGAGGAGAGAAACCAAGAGAGATCTCAAGTAGCCCATGTTTGTG 1

RESULT 6

CK252271/c

LOCUS

DEFINITION

EST735908 potato callus cDNA library, normalized and full-length

Solanum tuberosum cDNA clone POCB787 5' end, mRNA sequence.

ACCESSION

CK252271

VERSION

CK252271.1 GI:39806102

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

REFERENCE

1 (bases 1 to 899)

EuKaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

AUTHORS

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

TITLE

Generation of ESTs from potato callus tissue

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: EST735909

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

Location/Qualifiers

1..899

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POCB787"

/tissue_type="callus"

/lab_host="DH10B-RonA"

/clone_lib="potato callus cDNA library, normalized and full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 29.3%; Score 468.6; DB 14; Length 899;

Best Local Similarity 88.8%; Pred. No. 2.7e-87;

Matches 530; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

Qy 46 GGTATCTTTGTTGAAAATTTGAAAGACGTAGGACACATGGACCTTGGTGCAAC 105

Db 596 GGCATCTTTGTTGAAAATTTGAAAGACGTAGGACACATGGACCTTGGTGCAAC 537

Qy 106 AATATTGTTGCTCCCAATGTGTACAAAGATTGTTACATCCCTCGGGTACTTTAAGCT 165

Db 536 AATATTGTTGCTCCCGACGTGTACAAAGATTGTTACATCCCTCGAGGTACCTTAAGT 477

Qy 166 GACTAGGACATTCACCATTTATTTGCGGTGCAATGAATGTGTGCAATTCCTCCAC 225

Db 476 AACCAGGACATTCACCATTTATATTAGCCGTGCAATGAATGTGTGCAATTCCTCCAC 417

Qy 226 TTGGATTAGTCGGGGCGAAGTCATCGGTATTTAATTAATCCATCACTAAGAAATGTC 285

Db 416 TAGAATTTGTTGGGGCGAAGTCATCGGTATTTAATTAATCCATCACTAAGAAATGTC 357

Qy 286 AGAAATCTAAGTTGTTGAACCTGTTCCAAAGCGTACTCGGTAGGGTGTGTTGGTGTTC 345

Db 356 AGAAATCTAAGTTGTTGAACCTGTTCCAAAGCGTACTCGGTAGGGTGTGTTGGTGTTC 297

Qy 346 CCCACCCGGTGCACTGCGAGGACACCAACCAATCACCAGTCATGCGACCACTCTACCAG 405

Db 296 CCCACCCGGTACACTCGAAGACCCCAACCAATCACCAGTCTCGCATGAACCTCTACCAG 237

Qy 406 CACACCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCG 465

Db 236 CACCATCAAGTTGCAATTAGTACGACCCCATATAGTGCATCGTAGTGCCTTAGGCG 177

Qy 466 CATCAATGACCCACATTTGGCCCTCGATCGAGACGTGGGCGACCGCTATC-GGGTGGATG 524

Db 176 CATTGATAACCCATGTCTGGCCCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATG 117

Qy 525 CCSCCCAAAGCATGTATGGACAGTTCTTGGCGGTACTCGATAGTGCAGCAGTAAAGTAA 584

Db 116 CCSCCCACACGGTGTATGGACAGTTATTG--CGTACCTCGATAGTGGCAGCATAAAGTGA 59

Qy 585 AGTCACAAAAGCCAGAGGAGAGAAACCAAGAGAGATCTCAAGTAGCCCATGTTTGT 641

Db 58 AGTCACAAAAGCCAGAGGAGAGAAACCAAGAGAGATCTCAAGTAGCCCATGTTTGT 2

RESULT 7

BI176339/c

LOCUS

DEFINITION

EST521129 P. infestans-challenged potato leaf, compatible reaction

Solanum tuberosum cDNA clone PFCAC11 5' sequence similar to semotin-like protein [Capsicum annuum], mRNA sequence.

ACCESSION

BI176339

VERSION

BI176339.1 GI:14642150

KEYWORDS

EST.

SOURCE

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum

REFERENCE

1 (bases 1 to 739)

EuKaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

AUTHORS

Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chieming, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.

TITLE

Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: <http://genome.arizona.edu/orders/>

Seq primer: M13P-R.

FEATURES

Location/Qualifiers

1..739

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="PFCAC11"

/tissue_type="leaf"

/dev_stage="6 week old"

/lab_host="SOLP"

/clone_lib="P. infestans-challenged potato leaf, compatible reaction"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN

Query Match 29.1%; Score 465.2; DB 12; Length 739;
 Best Local Similarity 88.9%; Pred. No. 1.4e-86;
 Matches 526; Conservative 0; Mismatches 63; Indels 3; Gaps 2;

QY 46 GGTATCTTTGTTTGAAGAAATTTGAAAGAAAGTGGAGGACACATGAGACCTTGGGTGCAAC 105
 DB 590 GGCATCTTTGTTGAAATAATCTGACAAATCAGTAGGACACATGAGACCTTGGGTGCAAC 531

QY 106 AATATGTTGCTCCAAATGTTGTTCAAGATGTTTACATCTCCGGGTACTTTAAGCT 165
 DB 530 AATATGTTGCTCCAAATGTTGTTCAAGATGTTTACATCTCCGGGTACTTTAAGCT 471

QY 166 GACTAGGACATTCACATTTATTTTCCGCTGCAATGAATGTTGTCATTTCCCTCCAC 225
 DB 470 AACGAGGACATTCACATTTATTTAGCCGTGCATGAATGTTGTCATTTCCCTCCAC 411

QY 226 TTGATTAGTCCGGGCGAAAGTCACTCGGTATATTTAAATCCATCAACTAAAGAAATGTCCC 285
 DB 410 TAGGATTGTTGGGCGAAAGTCACTCGGTATATTTAAATCCATCAACTAAAGAAATGTCCC 351

QY 286 AGAATCTAAGTTGTTGAACTGTTCCAAAGGTTACTCGGTAGGTTTGGTGGTTTC 345
 DB 350 AGAATCTAAGTTGTTGAACTGTTCCAAAGGTTACTCGGTAGGTTTGGTGGTTTC 291

QY 346 CCCACCCGGTGCATCGAGGACACCAACAATCACCAGTCATGCACGAACTCTACCCAG 405
 DB 290 CCCACCCGGTGCATCGAGGACACCAACAATCACCAGTCATGCACGAACTCTACCCAG 231

QY 406 CACCAACGAGTTACATCCAGTACGACCCCATATATGTCGATCGTGTGCTTGGTGGTTC 465
 DB 230 CACCATCAAGTTACATCCAGTACGACCCCATATATGTCGATCGTGTGCTTGGTGGTTC 171

QY 466 CATCAATGACCCCATTTGGCTCGATCGAGAGCTCGGGGACCCCTATC-GGTCGATG 524
 DB 170 CATGATGACCCCATTTGGCTCGATCGAGAGCTCGGGGACCCCTATC-GGTCGATG 111

QY 525 CCGCCCAACGATGATGACAGTTGTTGGGGTACCTCGATAGTGCACGATGAAAGTGA 584
 DB 110 CCGCCCAACGATGATGACAGTTGTTGGGGTACCTCGATAGTGCACGATGAAAGTGA 53

QY 585 AGTCACAAAGCCAGAGGAGGAAACCAAGAGATCTCAAGTAGCCCATG 636
 DB 52 AGTCACAAAGCCAGAGGAGGAAACCAAGAGATCTCAAGTAGCCCATG 1

RESULT 8
 AW039873/c
 LOCUS
 DEFINITION EST282346 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET13J13, mRNA sequence.
 ACCESSION AW039873
 VERSION AW039873.1 GI:5898627
 SOURCE EST.
 ORGANISM Lycopersicon esculentum (tomato)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 649)
 D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, P., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato leaf tissue
 Unpublished (1999)
 CONTACT CUGI
 CLEMSON UNIVERSITY
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 Location/Qualifiers
 1..649

TITLE
 JOURNAL
 COMMENT

REFERENCES
 AUTHORS

FEATURES
 source

/organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Rio Grande PtoR"
 /db_xref="taxon:4081"
 /clone="cLET13J13"
 /tissue_type="leaf"
 /dev_stage="4-6 week old plants"
 /lab_host="XLI-Blue XRF"
 /clone_lib="tomato mixed elicitor, BTI"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLET - inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotin acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 28.6%; Score 456.6; DB 9; Length 649;
 Best Local Similarity 87.9%; Pred. No. 9.2e-85;
 Matches 521; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

QY 49 ATCTTTGTTTGAAGAAATTTGAAAGAAAGTGGAGGACACATGAGACCTTGGGTGCAACAT 108
 DB 591 ATCTTTGTTTGAAGAAATTTGAAAGAAATTTGAAAGAAAGTGGAGGACACATGAGACCTTGGGTGCAACAT 532

QY 109 ATTGTTGCTCCCAAAATGTTGTTTACATCTCTCCGGGTACTTTAAGCTGAC 168
 DB 531 ATTGTTGCTCCCAAAATGTTGTTTACATCTCTCCGGGTACTTTAAGCTGAC 472

QY 169 TAGGACATTCACATTTATTTGCGGTGCAATGAAATGTTGTCGATTTCCCTCCACTTG 228
 DB 471 CAGGACATTCACATTTATTTAGCCGTACAAATGAATTTGCAATGTCATTTCCCTCCACTTG 412

QY 229 GATTAGTCGGGCGAAAGTCACTCGGTATATTTAAATCCATCAACTAAAGAAATGTCCAGA 288
 DB 411 GATTAGTCGGGCGAAAGTCACTCGGTATATTTAAATCCATCAACTAAAGAAATGTCCAGA 352

QY 289 AATCTAAGTTGTTGAATCTGGTCCAAAGGCTACTCGGTAGGGTGTGTTGGTGGTGGCC 348
 DB 351 AATCTAAGTTGTTGAATCTGGTCCAAAGGCTACTCGGTAGGGTGTGTTGGTGGTGGCC 292

QY 349 ACCCGGTCGATCGAGGACACCAACAATCACCAGTCATCGACGAACTCTACGACAC 408
 DB 291 ACCCGGTCGATCGAGGACACCAACAATCACCAGTCATCGACGAACTCTACGACAC 232

QY 409 CACCGAAGTTACATCCAGTACGACCCCATATATACGTGCGATCTAGTGCCTTAGCGCGAT 468
 DB 231 CATCAAGTTGCAATTCGTACGACCCCATATATACGTGCGATCTAGTGCCTTAGCGCGAT 172

QY 469 CAATGACCCCATTTGGCTCGATCGAGACCTCGGGACCGCCTA-TCGGGTGCGATGCG 527
 DB 171 TGATGACCCCATTTGGCTCGATCGAGACCTCGGGACCGCCTA-TCGGGTGCGATGCG 112

QY 528 CCCAAACGATGTATGACAGTTGTTGGGCGTACCTCCATAGTGCAGCATAGTGAAGT 587
 DB 111 CCCGACCGGTATGACAGTTGTTGGGCGTACCTCCATAGTGCAGCATAGTGAAGT 54

QY 588 CACAAAAGCCGAGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTG 640
 DB 53 CACAAAAGCCGAGGAGAAACCAAGAGATCTCAAGTAGGCCATGTTTG 1

RESULT 9

BI432833/c
 LOCUS
 DEFINITION EST535594 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCAW35 5' sequence, mRNA sequence.
 ACCESSION BI432833
 VERSION BI432833.1 GI:15257523
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 583)

REFERENCE
AUTHORS Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.
TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
JOURNAL Unpublished (2000)
COMMENT Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES

Location/Qualifiers

1..583

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="PPCAW35"

/tissue_type="leaf"

/dev_stage="6 week old"

/lab_host="SOLR"

/clone_lib="P. infestans-challenged potato leaf,

compatible reaction"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."

ORIGIN

Query Match 28.5%; Score 455.2; DB 12; Length 583;
Best Local Similarity 88.7%; Pred. No. 1.8e-84;
Matches 516; Conservative 0; Mismatches 63; Indels 3; Gaps 2;
Qy 67 TGGAAAGACGTAGGACCATGGACCTTGGGTGCAACATATTTGTCTTCAATG 126
Db 581 TCGACAAATAGTAGGACCATGGACCTTGGGTGCAACATATTTGTCTTCAATG 522
Qy 127 TGGTACAGGATTGTACATCTCCGGGTACTTTTAAAGTCACTAGGACATTCAACATTTA 186
Db 521 TGGTACAGGATTGTACATCTCCAGGTACCTTAAGTGAACAGGACATTCAACATTTA 462
Qy 187 TATTTCGGTGCATTGAATTGTGGCATTTCCCTCCACTTGGATTAGTCGGGCGAAG 246
Db 461 TATTAGCGTGCAATGAATTGCGTGACATTTCCCTCCACTAGGATTGGTTGGGCGAAG 402
Qy 247 TCATCGGTATATTAATCACTCACTAAGAAATGTCAGAAATCAAGTTGTGAAT 306
Db 401 TCATCGGATATTAATCACTCACTAAGAAATGTCAGAAATCAAGTTGTGAAT 342
Qy 307 GGTCCAAGCGTACTCGGTAGGTGTTTGGTGTGTTTGCCTCCAGTGCACATTCGAGGA 366
Db 341 GGTCCAAGCGTACTCGGTAGGTGTTTGGTGTGTTTGCCTCCAGTGCACATTCGAGGA 282
Qy 367 CACACGACATCACTACGATGACGACGACCTTACGAGACGACCGAAGTTACATCCAG 426
Db 281 CCCCACCAATCACTACGATGACGACGACCTTACGAGACGACCGAAGTTACATCCAG 222
Qy 427 TACGACCCCATATACGTGCCATTCGTAGTGCCTTACGAGGATCAATGACCCACATTTGGC 486
Db 221 TACGACCCCATATACGTGCCATTTAGTACCCCTCGGGGCAATGATGACCCATGCTGGC 162

Qy 487 CTCGATCGAGACGTGGGACCGCCTATC-GGGTCGATCCGCCAAACGATGTATGGAC 545
Db 161 CTCGATCGAGACGTGGACACCGCCTATCGGGTGTGATCGCCACACGGTGTATGGAC 102
Qy 546 AGTTGTTGGGTACTCTGATAGTACACATAGTGAAGTCAAAAAGCCAGAGGGA 605
Db 101 AGTTGTTG--CGTACCTGATAGTGGCAGCATAGTGAAGTCAAAAAGCCAGAGGAA 44
Qy 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT 647
Db 43 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTTGTAACT 2

RESULT 10

LOCUS

DEFINITION

EST463582 tomato crown gall Lycopersicon esculentum cDNA clone CTOE1A9 5' sequence similar to putative pathogenesis-related protein PR P23, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta;

asterids; lamids; Solanales;

1 (bases 1 to 639)

van der Hoeven, R., Sun, H.,

Ronning, C. and Tanksley, S.

Generation of ESTs from tomato crown gall tissue

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES

Location/Qualifiers

1..639

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CTO81A9"

/tissue_type="crown gall"

/dev_stage="crown galls from full-grown plants (8 wks old)"

/lab_host="SOLR"

/clone_lib="tomato crown gall"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; Four wk old greenhouse plants were stab inoculated

on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr,

Cornell U.). Galls were allowed to develop for another 4

wks, when gall tissue was frozen in liquid nitrogen."

ORIGIN

Query Match 28.3%; Score 451.6; DB 12; Length 639;
Best Local Similarity 87.8%; Pred. No. 1e-83;
Matches 516; Conservative 0; Mismatches 69; Indels 3; Gaps 2;
Qy 49 ATCTTTGTTGAAAAAATTGGAAAGACGTAGGACCAATGGACCTTGGGTGCAACAAT 108
Db 587 ATCTTTGTTGAAAAAATCTCGACAAATCATAGTGGGCCACATGGACCTTGTGTGCAACAAT 528
Qy 109 ATTGTTGTCTCCCAATGTGTACAGGATTGTATCATCTCCGGTACTTTTAAAGCTGAC 168
Db 527 ATTGTTGTCTCGAAGCGTGTACAGGATTGTATCATCTCCGGTACTTCCCTAAGTGAAC 468
Qy 169 TAGGACATTCAACATTATATTTCGCGTGCATTGAATTGTGTGGCAATTTCCCTCCACTTG 228
Db 467 CAGGACATTCAACATTATATTAGCGGTACAATGAATTGCATGGCAATTTCCCTCCACTAG 468
Qy 229 GATTAGTCGGGGGGAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCCGA 288

[illegible]

RESULT 11	BI922472	667 bp	mRNA	linear	EST 17-OCT-2001
LOCUS	BI922472/c	ES1542376	tomato callus Lycopersicon esculentum	cdNA clone	
DEFINITION		CFE77J15 5' end, mRNA sequence.			
ACCESSION	BI922472				
VERSION	BI922472.1	GI:16219560			
KEYWORDS	EST.				
SOURCE	Lycopersicon esculentum (tomato)				
ORGANISM	Lycopersicon esculentum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.				
REFERENCE	1 (bases 1 to 667)				
AUTHORS	Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Renning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.				
TITLE	Generation of ESTs from tomato callus tissue (2001)				
JOURNAL	Unpublished (2001)				

FEATURES source

```

institute
seq primer: T3.
Location/Qualifiers
1. .667
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC77J15"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP,"
/clone_lib="tomato callus"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

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ORIGIN	Query Match Best Local Similarity Matches 520; Conservative	28.1%; Score 449.6; DB 12; Length 667; 86.4%; Pred. No. 2.6e-83; 0; Mismatches 79; Indels 3; Gaps 2;
QY	47	GTATCTTGTCTTTGAAGAAATTCGAAAGAACGCTAGGACACACATGCACCTTGGTGCACA 106
DB	601	GGACATCTTGTGTGAAGAAATCTCGACAAATCAGTAGGGCCACATGACCTTGTGTGCAACA 542
QY	107	ATATTCTTGTCTCTCCAAATGTGTGTAACAGGATTTTACATCCTCCGGGTACTTTAAGCTG 166
DB	541	ATATTCTTGTCTCTCGAAGCTGTGTACAAGGATTTTACATCCTCCGGGTACCTAAGTGA 482
QY	167	ACTAGACATTCACANTTTATTTTGCCTGTGATTTGAATGTGTGTGGCATTTCCCTCCACT 226
DB	481	ACCAGACATTCACCATTTTATATTAGCCGTACAATGAATTGATGGCATTTCCCTCCACT 422
QY	227	TGGATTAGTCGGGGGAAAGTTCATCGGTATATAAATCCATCAACTAAAGAAATGTCCCA 286
DB	421	AGGATTGCTCGGGGCGAAAGTTCATTTGAATATATTAATCCATCGACTAAGAAATGTCCCA 362
QY	287	GAAATCTAAGTTGTTGAACTGTTCCAAAGCGTACTCGGCTTAGGGTGTTTTGGTGGTTGCC 346
DB	361	GAAATCTAGGTTGCTAAACTGTTGCCAAAGCGTACTCGGCCAGGGTGTTTTGGTGGTTGCC 302
QY	347	CCACCGGTGTACTCGAGACACCCACCAATCACCAAGTCATGACGACCTCTACCAGC 406
DB	301	CCACCCGGTACATTGCAAGACCCACCAATCACCAAGTCTGACATGAACCTCTACCAGC 242
QY	407	ACCACCGAAGTTACATCCAGTAGCAGCCCATATACGTGCCATCGTAGTGCCCCCTAGGCGC 466
DB	241	ACCATCAAAGTTGCAATTCTGTACGACCCCATATACGTGCCATCTTAGTCCCCCTCGGTGC 182
QY	467	ATCAATGACCCACATTTGGCCTCGATCGAGACGTGGGACCGCCCTA-TCGGGTGATGC 525
DB	181	ATTGATGACCCCATGTTTGGCCTTCGATCAAGACGTGCACCCGCCTATTGGGGTGCACGC 122
QY	526	CGCCCCAAACGATGTATGGACAGTTGTTTGGCGGTAGCTCGATAGTGACAGCATAAAGTGAAA 585
DB	121	CGCCACAGCGGTATATGNACAGTTGTTG--CGTACCTCGAAAGTGGCAGCATAAAGTGTA 64
QY	586	GTCAAAAGCCAGAGGAGGAGAAACCAAAAGAAAGATCTCAAGTAGCCCATGTTTGTGAA 645
DB	63	GTCAAAAGCAAGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGGCCCATGTTTGTGGAA 4
QY	646	AT 647

RESULT 12	
BF053678/c	
LOCUS	
DEFINITION	622 bp mRNA linear EST 07-MAR-2003
	EST438908 potato leaves and petioles Solanum tuberosum cDNA clone
	CST336B20 5' sequence, mRNA sequence.
ACCESSION	
VERSION	BF053678
KEYWORDS	
SOURCE	BF053678.1 GI:10807574
ORGANISM	EST.
	Solanum tuberosum (potato)
	Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
asterids; lamids; Solanales; Solanaceae; Solanum.	
1 (bases 1 to 622)	
van der Hoeven,R.S., Bezzerides,J., Holt,I.B., Liang,F., Cho,J.,	
Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R.,	
Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.	
Generation of ESTs from potato leaves and petioles	
Unpublished (2000)	
TITLE	Contact: Robin Buell
JOURNAL	The Institute for Genomic Research
COMMENT	9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.

FEATURES

source
1..622
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSPB36820"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/clone_lib="potato leaves and petioles"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN

Query Match 28.1%; Score 449; DB 10; Length 622;
Best Local Similarity 86.9%; Pred. No. 3.5e-83;
Matches 517; Conservative 0; Mismatches 75; Indels 3; Gaps 2;
QY 46 GGTATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGCGCTGGGTGCAAC 105
Db 602 GGCATCTTTGTTGAAAAATCTCGACCACTCAGTAGGACCAATGCGCTGGGTGCAAC 543
QY 106 AATATGTTGCTCCCAATGTTGACAGGATTTTACATCTCCGGGTACTTTAGCT 165
Db 542 AATATGTTGCTCTGACGCTGGTACAGGATTTTACATCTCCGGGTACTTTAGCT 483
QY 166 GACTAGGACATTCACCAATTTATTTGCGGTGATTTGAATTTGTTGCAATTTCCCTCCAC 225
Db 482 GACCAAGGCAATTCACCAATTTATTTGCGGTGATTTGAATTTGTTGCAATTTCCCTCCAC 423
QY 226 TTGATTTAGTCCGGGCGAAAGTCATTCGGTATATTTAAATCCATCAACTAAAGAAATGCC 285
Db 422 TAGGATTTGCTCGGGGCAAAAGTCATTTGGTATATTTAAATCCGCTCACTAAAGAAATGCC 363
QY 286 AGAATCTTAAGTTGTTGAACCTGTTCCAGGCGTACTCGGTGAGGTGTTGGTGGTTTC 345
Db 362 AGAATCTTAAGTTGTTGAACCTGTTCAAGGCAATTTGCGCCAGGTTGTTGGCGTTTAC 303
QY 346 CCCACCGGTGCTGACGACGACCAACCAATCACCAGTCAAGCAGCAACCTCTACCAAG 405
Db 302 CCCACCGGTGCTGACGACGACCTCAACCAATCACCAGTCTGACAGAACTCTACCAAG 243
QY 406 CACCACGAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTAGCGG 465
Db 242 CACCATCAAGTTGCAATTTAGTACGACCCCATATACGTGCGCATCTTAGTCCCTCGGTG 183
QY 466 CATCAATGACCCCATTTGGCTCGATCGAGACCTGCGGACCCGCTATC-GGGTCGATG 524
Db 182 CATTTAGTACCCCAAGTTGACCTCGATCGAGCTGCGGACCCGCTATCGGGTTCATG 123
QY 525 CCGCCCAAAACGATGTATGACAGTTGTTGGCGGTACCTCGATGATGACGATTAAGTGAA 584
Db 122 CCGCCCAAGCGGTGTATGACAGTTGTT--TCGGACCTCAAAAGAGGTAGCATTAAGTATA 65
QY 585 AGTCACAAAGCCAGAGGGAGAAACCAAAAGAGATCTCAAGTAGCCCATGTTT 639
Db 64 AGTCACAAAGAGAGGAGAGAAACCAAAAGAAATCTCAATAGCCCATGTTT 10

RESULT 13

AW031249/c

LOCUS

DEFINITION ES2274624 tomato callus, TAMU lycopersicon esculentum cDNA clone
cLEC34F24 similar to osmotin-like protein TPM-1 precursor (PR F23),

ACCESSION

AW031249

VERSION

AW031249.1

GI:5889926

KEYWORDS

EST.

SOURCE

Lycopersicon esculentum (tomato)

ORGANISM

Lycopersicon esculentum

REFERENCE

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Kolt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)

AUTHORS

Clemson University Genomics Institute

TITLE

Clemson University

JOURNAL

100 Jordan Hall, Clemson, SC 29634, USA

COMMENT

Email: http://www.genome.clemson.edu/orders/index.html

FEATURES

Location/Qualifiers

1..585

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="cLEC34F24"

/tissue_type="callus"

/dev_stage="25-40 days old"

/lab_host="XL1-Blue MRP"

/clone_lib="tomato callus, TAMU"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato callus EST Library"

ORIGIN

Query Match 28.0%; Score 447.2; DB 9; Length 585;
Best Local Similarity 87.5%; Pred. No. 8.5e-83;
Matches 511; Conservative 0; Mismatches 70; Indels 3; Gaps 2;
QY 67 TGGAAAGAACGTAGGACCAATGAGACCTTGGGTGCAACAATATTTGTTCTCCAAATG 126
Db 583 TCGACAAATCAGTAGGNCACATGGACCTTGTGTGCAACAATATTTGTTCTCCGAAAG 524
QY 127 TGGTACAAGGATTTTACATCTCCGGGTACTTTAAGCTGACTAGGACATTCACCAATTTA 186
Db 523 TGGTACAAGGATTTTACATCTCCGGGTACTCCNAAAGTGAACACGACATTCACCAATTTA 464
QY 187 TATTTCCGTGCAATGAATTTGTGTGCAATTTCCCTCCACTTGGATTTAGTCGGGGGAAAG 246
Db 463 TATTAGCCGTACAATGAATTTGCATGTCATTTCCCTCCACTAGGATTTGGTCGGGGGAAAG 404
QY 247 TCATCGGTATATTAATCCATCACTAAAGAAATGTCACAGAAATCTAGATTTGTTGAATC 306
Db 403 TCATCGGAATATTAATCCATCACTAAAGAAATGTCACAGAAATCTAGATTTGTTGAATC 344
QY 307 GGTCCAAGCGTACTCGGCTAGGGTGTGTTGGTGGTTTGGCCACCCGCTGCTACGAGA 366
Db 343 GGTCCAAGCGTACTCGGCGAGGGTGTGTTGGTGGTTTGGCCACCCGCTGCTACGAGA 284
QY 367 CACCACCAATCAACGATTCAGCAACCTTACAGCACACCGAAGTTACATCCAG 426
Db 283 CCCCACCAATCAACGATTCAGCAACCTTACAGCACACCGAAGTTACATCCAG 224
QY 427 TAGACCCCATATACGTGTCATCTAGTCCCTCCTAGGCGCATCAATGACCCACATTTGGC 486
Db 223 TAGACCCCATATACGTGTCATCTAGTCCCTCCTCCTCGGTGCATGATGACCCCATTTGGC 164

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QY 487 CTCGATCGAGAGCTCGGGCCCGCCTA-TCGGGTCGATGCGGCCCAACAGATGTATGGAC 545
Db 163 CTCGATCAAGAGCGTCGACCCCGCTATTGGGTCGACGCGCCGACGCTGTATGGAC 104
QY 546 AGTTGTTGGCGGTACCTCGATAGTCAGATAGTGAAGTCAAAAAGCCAGAGGGA 605
Db 103 AGTTGTTG--CGTACCTCGAAGTGGCGATAGTGAAGTCAAAAAGCCAGAGGGA 46
QY 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT 649
Db 45 GAAACCAAAAGAGATCTCAAGTAGGCCATGTTGTTGGAATAT 2

RESULT 14
AW032915/c
LOCUS EST276474 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC16P23, mRNA sequence.
ACCESSION AW032915
VERSION AW032915.1 GI:5891671
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 583)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
source
Location/Qualifiers
1..583
/organism="Lycopersicon esculentum"
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/clone="cLEC16P23"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XU1-Blue MRF"
/clone_lib="tomato callus, TAMU"
/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

ORIGIN
Query Match 27.6%; Score 440.8; DB 9; Length 583;
Best Local Similarity 87.1%; Pred. No. 1.8e-81;
Matches 507; Conservative 0; Mismatches 72; Indels 3; Gaps 2;

QY 67 TGGAAAGACGTAGGACACCATGGACCTTGGGTGCAACAATATGTTGCTCCAAATG 126
Db 581 TCGACAATCAGTAGGGCCACATGGACCTTGTGTGCAACAATATGTTGCTCCGAAAG 522
QY 127 TGGTACAGGATTTGATCATCTCCGGGTACTTTAGCTGACATGACATTCACCATTTA 186
Db 521 TGGTACAGGATTTGTTACATCTCCGGGTACCTGAGTGAACGACATTCACCATTTA 462
QY 187 TATTGCGCGTCATGTAATTTGTGTGGCATTTCCCTCCACTGTGATTCGGGGCGAAAG 246
Db 461 TATTAGCCGTACAATGAATTGCATGGCATTTCCCTCCACTGATGTTGGTTCGGGGCGAAAG 402

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QY 247 TCATCGGTATATTAAATCCATCAACTAAGAAATGTCCAGAAATCTAAGTTGTGAAC 306
Db 401 TCATTGGAATATTAAATCCATCGACTAAGAAATGTCCAGAAATCTAAGTTGTGAAC 342
QY 307 GGTCCAAAGCGCTACTCGGCTAGGCTGTTGGTGTGTTGCCCGCCCGGTGCACATG 366
Db 341 GGTCCAAAGCGCTACTCGGCTAGGCTGTTGGTGTGTTGCCCGCCCGGTGCACATG 282
QY 367 CACCACCAATCAATCAGTCTATGCACGAACCTCTACAGCAGCCACCGAAGTATCAT 426
Db 281 CCCCACCAATCAATCAGTCTATGCACGAACCTCTACAGCAGCCACCGAAGTATCAT 222
QY 427 TAGGACCCCATATAGTCTCCATCGTCCATCGTCCCTTAGGGGATCAATGACCATTT 486
Db 221 TAGGACCCCATATAGTCTCCATCGTCCATCGTCCCTTAGGGGATCAATGACCATTT 162
QY 487 CTCGATCGAGAGCTCGGGCCCGCCTA-TCGGGTCGATGCGGCCCAACAGATGTAT 545
Db 161 CTCGATCGAGAGCTCGGGCCCGCCTA-TCGGGTCGATGCGGCCCAACAGATGTAT 102
QY 546 AGTTGTTGGCGGTACCTCGATAGTCAGATAGTGAAGTCAAAAAGCCAGAGGGA 605
Db 101 AGTTGTTG--CGTACCTCGAAGTGGCGATAGTGAAGTCAAAAAGCCAGAGGGA 44
QY 606 GAAACCAAAAGAGATCTCAAGTAGCCCATGTTGTTGAAAT 647
Db 43 GAAACCAAAAGAGATCTCAAGTAGGCCATGTTGTTGGAAT 2

CK273930 923 bp mRNA linear EST 12-DEC-2003
EST720008 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POADE25 5' end, mRNA sequence.

ACCESSION CK273930
VERSION CK273930.1 GI:39830908
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 923)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST720009
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
Location/Qualifiers
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/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POADE25"
/tissue_type="abiotic stress treated leaf and root tissue"
/clone_lib="potato abiotic stress cDNA library"
/note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and then
Set 2 were grown under the standard conditions and then

```

were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match	27.5%;	Score 439.2;	DB 14;	Length 923;
Best Local Similarity	85.6%;	Pred. No. 3.5e-81;		
Matches 512;	Conservative 0;	Mismatches 83;	Indels 3;	Gaps 2;
Qy	46	GGTATCTTTGTTGAAAAAATTTGAAAAAGACGTAGGACACATGGACCTTGGGTGCAAC	105	
Db	601	GGCATCTTTTCTGAAAAAATTTGACAACTCTGTAGACACATGGACCTTGGGTGAGC	542	
Qy	106	AATATGTTGTCCTCCAAATGTGTACAGGATTTGATATCTCTCCGGGTACTTTAAGCT	165	
Db	541	AATATGTTGTCCTCCGAAATGTGTACAGGATTTGATATCTCTCCAGGTACCTTAAGG	482	
Qy	166	GACTAGGACATCCATTATATTTGCGTGCATTTGAATTTGTGGCATTTCCCTCCAC	225	
Db	481	CGCAGGACATCCATTATATTTGCGGTGCAATGAATTTGATGATTTCCAGCAC	422	
Qy	226	TTGGATTAGTCGGGGCGAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGCCC	285	
Db	421	TAGGTTTGGTTGGGCAAAAGTCATTGGAATATTGAATCCGTCAACTAAAGAAATATCCC	362	
Qy	286	AGAAATCTAAGTTGTTGAACTGGTCCAGGCGTACTCGGCTAGGGTGTTTGGTGGTTGC	345	
Db	361	AGAAATCTAGGTTGCTAAACTGATCCAAAGGCATATTCAGCCAAAGGTGTTTGGGGGCTGC	302	
Qy	346	CCCACCGGTGCACCTGCAGGACACCCACCAATCACAGTCATGCACGAACCTCTACCA	405	
Db	301	CCCACCGGTACATGCAAGACTCCACCAATCACAGTCATGCACGAACCTCTACCA	242	
Qy	406	CACCAACGAAGTTACATCCAGTAGACCCCATATACGTGCCATCGTAGTGCCTTAGGCG	465	
Db	241	CAGCATTTGAAGTTACAAACAGTAGACCCCATATACGTGCCATCTTAGTTCCTCCCTGGAG	182	
Qy	466	CATCAATGACCCACATTTGGCTCGATCGAGACGTGCGGACCCGCTATC-GGGTCGATG	524	
Db	181	CATTGATGACCCATGTTTGGGCTTTATTGAGACGTGCGACCCGCTATCGGGGTGATG	122	
Qy	525	CCGCCAAACGATGTATGACAGTTGTTGGCGGTACCTCGATAGTAGACAGCATTAAGTAA	584	
Db	121	CTGCCCAACAGGTGTATGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATTAAGTAA	64	
Qy	585	AGTCACAAAGCCGAGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTGTT	642	
Db	63	AGTCACAAAGCAGAGGAGGAGAACCAAAAGAGATCTCAAGTAGCCCATGTTTAAAT	6	

Search completed: August 18, 2004, 16:04:24
Job time : 3758.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 07:30:51 ; Search time 679.862 Seconds
(without alignments)
11157.588 Million cell updates/sec

Title: US-10-051-307-3

Perfect score: 1546

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1545	99.9	1546	US-10-051-307-3	Sequence 3, Appli
2	1362.4	88.1	1595	US-10-051-307-1	Sequence 1, Appli
3	1334.4	86.3	1598	US-10-051-307-2	Sequence 2, Appli
C 4	291.2	18.8	510	US-10-341-961A-371	Sequence 371, App
C 5	207.2	13.4	735	US-09-938-842A-2118	Sequence 2118, Ap
C 6	207.2	13.4	735	US-09-938-842A-2118	Sequence 2118, Ap
C 7	207.2	13.4	950	US-09-770-445-334	Sequence 334, App
C 8	182.4	11.8	909	US-10-424-599-103619	Sequence 103619,
C 9	180.6	11.7	875	US-10-636-396-4	Sequence 4, Appli
C 10	180.6	11.7	875	US-10-636-396-4	Sequence 4, Appli
C 11	171.6	11.1	1566	US-10-424-599-36321	Sequence 36321, A
C 12	155.8	10.1	1717	US-10-259-165-389	Sequence 389, App
C 13	155.8	10.1	720	US-10-259-165-41	Sequence 41, Appli
C 14	153.6	9.9	1006	US-10-437-963-86607	Sequence 86607, A

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C 15 145.4 9.4 1173 13 US-10-424-599-7736 Sequence 7736, Ap
C 16 142.6 9.2 696 15 US-10-259-165-353 Sequence 353, App
C 17 142.6 9.2 699 15 US-10-259-165-109 Sequence 109, App
C 18 142.6 9.2 1052 17 US-10-437-963-89569 Sequence 89569, A
C 19 140.6 9.1 1020 15 US-10-259-165-571 Sequence 571, App
C 20 140.6 9.1 1020 16 US-10-260-238-3136 Sequence 3136, App
C 21 135.6 8.8 805 16 US-10-260-238-4061 Sequence 4061, App
C 22 135.6 8.8 879 13 US-10-260-238-49 Sequence 49, Appli
C 23 135.4 8.8 901 13 US-10-424-599-7737 Sequence 7737, App
C 24 135.2 8.7 911 13 US-10-425-114-27634 Sequence 27634, A
C 25 135.2 8.7 922 16 US-10-260-238-4067 Sequence 4067, App
C 26 115.4 7.5 343 9 US-09-770-791-806 Sequence 806, App
C 27 112.8 7.3 1350 17 US-10-437-963-59877 Sequence 59877, A
C 28 109.4 7.1 3630 17 US-10-437-963-16245 Sequence 16245, A
C 29 104.4 6.8 808 9 US-09-966-881-46 Sequence 46, Appli
C 30 104.4 6.7 1928 13 US-10-425-114-24457 Sequence 24457, A
C 31 102.4 6.6 869 17 US-10-437-963-15621 Sequence 15621, A
C 32 102.4 6.5 633 15 US-10-259-165-532 Sequence 532, App
C 33 100.4 6.5 633 16 US-10-260-238-5182 Sequence 5182, App
C 34 94 6.1 621 15 US-10-175-389-1 Sequence 1, Appli
C 35 92.8 6.0 621 15 US-10-175-389-9 Sequence 25389, A
C 36 91.8 5.9 730 13 US-10-425-114-25389 Sequence 25389, A
C 37 91.8 5.9 826 13 US-10-425-114-23076 Sequence 23076, A
C 38 91.6 5.9 973 17 US-10-437-963-16928 Sequence 16928, A
C 39 88.8 5.7 728 16 US-10-260-238-3135 Sequence 3135, App
C 40 86 5.6 730 13 US-10-425-114-27495 Sequence 27495, A
C 41 83.4 5.4 904 13 US-10-425-114-28239 Sequence 28239, A
C 42 82.6 5.3 891 17 US-10-437-963-49328 Sequence 49328, A
C 43 81 5.2 721 13 US-10-425-114-2055 Sequence 2055, App
C 44 81 5.2 753 13 US-10-425-114-23100 Sequence 23100, A
C 45 81 5.2 807 13 US-10-425-114-15687 Sequence 15687, A

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ALIGNMENTS

RESULT 1

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US-10-051-307-3
; Sequence 3, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1546
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1248)
; OTHER INFORMATION: a, t, c or g
US-10-051-307-3

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Query Match 99.9%; Score 1545; DB 14; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATCTTTGTTGAAAAATTCGAAAGACATGACATGACCTTGGGTGCAACAT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ATCTTTGTTGAAAAATTCGAAAGACATGACATGACCTTGGGTGCAACAT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 ATTGTTCTCTCCAAATGTTGTTACATCTCCGGGTACTTTAAGTGAC 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ATTGTTCTCTCCAAATGTTGTTACATCTCCGGGTACTTTAAGTGAC 120
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QY 121 TAGGACATTCACCATTTATATTTGGCGTGCATTTGAATTTGGGTGGCAATTTCCCTCCACTTG 180
DB 121 TAGGACATTCACCATTTATATTTGGCGTGCATTTGAATTTGGGTGGCAATTTCCCTCCACTTG 180
QY 181 GATTAGTGGGGCGGAAAGTCATCGGTATATTAATTAATCCATCAACTAAAGAAATGTCGCCAGA 240
DB 181 GATTAGTGGGGCGGAAAGTCATCGGTATATTAATTAATCCATCAACTAAAGAAATGTCGCCAGA 240
QY 241 AATCTAAGTTGTTGAATCGGTCCGAGGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 300
DB 241 AATCTAAGTTGTTGAATCGGTCCGAGGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 300
QY 301 ACCCGGTGCATCGAGGACACCCACCAATCACCAGTCATGCGAGACCTCTACAGCAC 360
DB 301 ACCCGGTGCATCGAGGACACCCACCAATCACCAGTCATGCGAGACCTCTACAGCAC 360
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGAGTGCCTAGGCGCAT 420
DB 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGAGTGCCTAGGCGCAT 420
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTGCATGCTG 480
DB 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTGCATGCTG 480
QY 481 CCCGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
DB 481 CCCGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
QY 541 CAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 600
DB 541 CAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 600
QY 601 ATATGTGACAAATATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCACTA 660
DB 601 ATATGTGACAAATATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCACTA 660
QY 661 TGGATATTAATCGTATTATTAACAATATCATCTTTGACTAATTAATAACAATAATAT 720
DB 661 TGGATATTAATCGTATTATTAACAATATCATCTTTGACTAATTAATAACAATAATAT 720
QY 721 TACAAATATGTTTGGTAAAGTTGAGTGGCAAAATGTATAAGAGCGGCTATATATTA 780
DB 721 TACAAATATGTTTGGTAAAGTTGAGTGGCAAAATGTATAAGAGCGGCTATATATTA 780
QY 781 TTATTTTATGAATATAGACTATAGTTACAAAGTGAACCTTTATTTGGTCAATAACTTGACAT 840
DB 781 TTATTTTATGAATATAGACTATAGTTACAAAGTGAACCTTTATTTGGTCAATAACTTGACAT 840
QY 841 ATAACTCTGTATCGTGACGGAATTTTCTTAAACCTAAATATATAAAGACGCTATTTT 900
DB 841 ATAACTCTGTATCGTGACGGAATTTTCTTAAACCTAAATATATAAAGACGCTATTTT 900
QY 901 AATATTTTTCGTGGCCAAAGTTTCTGCACTATTTCTAGTGCCTTTTACTTTTATCG 960
DB 901 AATATTTTTCGTGGCCAAAGTTTCTGCACTATTTCTAGTGCCTTTTACTTTTATCG 960
QY 961 TTCTAGGCTTCTAGGTACGGTGTGAACATAAATAATCATAAATTTGAAGTAAATTT 1020
DB 961 TTCTAGGCTTCTAGGTACGGTGTGAACATAAATAATCATAAATTTGAAGTAAATTT 1020
QY 1021 AGTTTTTTTTCATATCTAGTATGATGATTTGTTAGATCAATGTGAATATACAAATC 1080
DB 1021 AGTTTTTTTTCATATCTAGTATGATGATTTGTTAGATCAATGTGAATATACAAATC 1080
QY 1081 ATTCTGATTTTAAATCATAACTATTCTGATGATGGGAACGCTCTATGGTGTATGCTGAC 1140
DB 1081 ATTCTGATTTTAAATCATAACTATTCTGATGATGGGAACGCTCTATGGTGTATGCTGAC 1140
QY 1141 AAGTGTGATTTTATCTAAGTCTGATTTGGAGTCAACACTTTTAGTGCAATATCTATT 1200
DB 1141 AAGTGTGATTTTATCTAAGTCTGATTTGGAGTCAACACTTTTAGTGCAATATCTATT 1200
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QY 1201 AAAAGAACCCCTATTGTATGCAAAAGTCAATAAATTAATTAATCATNCTTTATTATTT 1260
DB 1201 AAAAGAACCCCTATTGTATGCAAAAGTCAATAAATTAATTAATCATNCTTTATTATTT 1260
QY 1261 TTACGATCGGAGCATGGATACATTTACTTAATTAATAAATTTGGAAGAAATGATCGACA 1320
DB 1261 TTACGATCGGAGCATGGATACATTTACTTAATTAATAAATTTGGAAGAAATGATCGACA 1320
QY 1321 AGTCATCAAGCTTTATCGTCGATCCACATTCCTCCCTAACGTTAGTAGTGGCTGCTTTAGAGA 1380
DB 1321 AGTCATCAAGCTTTATCGTCGATCCACATTCCTCCCTAACGTTAGTAGTGGCTGCTTTAGAGA 1380
QY 1381 AACAGTGGATCATGTATTAATTTAGTTTCCCTATCTCTATAAATATCTATATATACC 1440
DB 1381 AACAGTGGATCATGTATTAATTTAGTTTCCCTATCTCTATAAATATCTATATATACC 1440
QY 1441 TCTAAAACTAAATGTCATCTAACACACAAATATAAATCTTAGATTTCTTTAAAGAAATTCGA 1500
DB 1441 TCTAAAACTAAATGTCATCTAACACACAAATATAAATCTTAGATTTCTTTAAAGAAATTCGA 1500
QY 1501 GAATTAATGAGGAGCAAAATAAGTCTATGTTGAAGTTGGTTGCTTTC 1546
DB 1501 GAATTAATGAGGAGCAAAATAAGTCTATGTTGAAGTTGGTTGCTTTC 1546

RESULT 2
US-10-051-307-1
; Sequence 1, Application US/10051307
; Publication No. US20020170095A1
; GENERAL INFORMATION:
; APPLICANT: DAI, ZIVU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
; FILE REFERENCE: 059440/0141
; CURRENT APPLICATION NUMBER: US/10/051,307
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,224
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-1

Query Match 86.1%; Score 1362.4; DB 14; Length 1595;
Best Local Similarity 94.1%; Pred. No. 3.5e-289;
Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

QY 1 ATCTTTGTTTCAAAAAATTGGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 60
DB 49 ATCTTTGTTTCAAAAAATTGGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 108
QY 61 ATTGTGTCCTCCAAATGTGTACAAGGATTTTACATCTCTCGGGTACTTTAAGCTGAC 120
DB 109 ATTGTGTCCTCCAAATGTGTACAAGGATTTTACATCTCTCGGGTACTTTAAGTTGAC 168
QY 121 TAGGACATTCACCATTTATATTTGGCGTGCATTTGAATTTGGGTGGCAATTTCCCTCCACTTG 180
DB 169 CAGGCAATTCACCATTTATATTTGGCGTGCATTTGAATTTGGGTGGCAATTTCCCTCCACTTG 228
QY 181 GATTAGTGGGGCGGAAAGTCAATCGGTATATTAATTAATCCATCAACTAAAGAAATGTCGCCAGA 240
DB 229 GATTAGTGGGGCGGAAAGTCAATCGGTATATTAATTAATCCATCAACTAAAGAAATGTCGCCAGA 288
QY 241 AATCTAAGTTGTTGAATCGGTCCGAGGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 300
DB 289 AATCTAAGTTGTTGAATCGGTCCGAGGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 348
QY 301 ACCCGGTGCATCGAGGACACCCACCAATCACCAGTCATGCGAGACCTCTACAGCAC 360
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Db 349 ACCGGTGCATCGAGGACACCAACATACAGTCATGACGAACTCTACCAGCAC 408
 Qy 361 CATCGAAGTTACATCCAGTAGAGACCCCATATAGCTGCCATCGTAGTGCCTTAGGCGCAT 420
 Db 409 CATCGAAGTTACATCCAGTAGAGACCCCATATAGCTGCCATCGTAGTGCCTTAGGCGCAT 468
 Qy 421 CAATGACCCAGTTTGGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTGCGATGCTG 480
 Db 469 CAATGACCCAGTTTGGCTCGATCGAGAGCGTGGCCACCGCTATCGGGGTGCGATGCTG 527
 Qy 481 CCCAGACGGTGTATGAGACAGTTTGGTACCTCGATGAGTGGGAGCATATAGTGAAGTCA 540
 Db 528 CCCAAGCGATGTATGAGACAGTTTGGTACCTCGATGAGTGGGAGCATATAGTGAAGTCA 587
 Qy 541 CABAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 600
 Db 588 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 647
 Qy 601 ATATGTGACAAATATATTTTGGTACTTATATATAGGATATGCGCGCTTTGGCACTA 660
 Db 648 ATATGTGACAAATATATTTTGGTACTTATATATAGGATATGCGCGCTTTGGCACTA 707
 Qy 661 TGGATATTAATCGTATATATAACAATATCATATCTTGTACTATATATATATATATATAT 720
 Db 708 CGGATATTAATCGTATATATAACAATATCATATCTTGTACTATATATATATATATATAT 767
 Qy 721 TACAATATGATTTCGTAAACGTTGAGTGGCAAAATGTATAAGACCGCCCTAATAATTA 780
 Db 768 TACAATATGATTTCGTAAACGTTGAGTGGCAAAATGTATAAGACCGCCCTAATAATTA 827
 Qy 781 TTATTTATGAATATAGACTATAGTCAAGTGAACCTTTATTTGGTGAATATCTTGGACAT 840
 Db 828 TTATTTATGAATATAGCTATAGTCAAGTGAACCTTTATTTGGTGAATATCTTGGACAT 887
 Qy 841 ATAACTCTGATCGTGAAGAACTTTCTTAAACTAAATATATAAAGCAGCTATTTT 900
 Db 888 ATAACTCTGATCGTGAAGAACTTTCTTAAACTAAATATATAAAGCAGCTATTTT 947
 Qy 901 AATATTTTCTGCGCAAGTTTCTGTCATATCTATATGCGCATTTTACTTTTATCG 960
 Db 948 CAGATTTTCTGCGCAAGTTTCTGTCATATCTATATGCGCATTTTACTTTTATCG 1007
 Qy 961 TTCTAGCCCTCTAGTACGCTTTGACATATAAATCATAAATTTGAAGTAAATTT 1020
 Db 1008 TTCTAGCCCTCTAGTACGCTTTGACATATAAATCATAAATTTGAAGTAAATTT 1067
 Qy 1021 AG-- --TTTTTTTTCATATATCTGATGATGATCTTTGTAGTCAATCTGGAATATACAA 1077
 Db 1068 AGTTTTTTTTTTCATATATCTGATGATGATCTTTGTAGTCAATCTGGAATATACAA 1127
 Qy 1078 ATCATCTGATTTTAAATATCATATCTTCTGATGATGAGGAACTGATGCTATCGT 1137
 Db 1128 ACCATCTGATTTTAAATATCATACCAATCTGCAAGGGGAAGTCTAT-- --GTGATCGT 1184
 Qy 1138 GACAGTCTGATTTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGAT 1197
 Db 1185 GACAGTCTGATTTTATTTTAAAGTCTGATGATGATGATGATGATGATGATGATGAT 1244
 Qy 1198 ATTTAAAGAACCCCTATTGATGCAAAAGTCAATAA-- --TATTTAATATATCTTTATT 1255
 Db 1245 ATTTAAAGAACCCCTATTGATGCAAAATATCTATTAAAGAACCCCTATTATCTTTATT 1304
 Qy 1256 TATTTTATGATCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315
 Db 1305 TATTTTATGATCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364
 Qy 1316 CGACAGTCAATCAAGCTTATCGTCAATCCCATTCCTTAAAGTATGATGATGATGATGAT 1375
 Db 1365 CGACAGTCAATCAAGCTTATCGTCAATCCCATTTAAAGTATGATGATGATGATGATGAT 1424
 Qy 1376 AGAGAAACAAAGTGAATCATGATATATTTAGTTTCCCTTCTCTCTATATATATATATAT 1435
 Db 1425 AGAGAAACAAAGTGAATCATGATATATTTAGTTTAAATATCTCTCTATATATATATATAT 1484

RESULT 3

US-10-051-307-2
 ; Sequence 2, Application US/10051307
 ; Publication No. US20020170095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DAI, ZIYU
 ; APPLICANT: SHI, LIFANG
 ; APPLICANT: HOOKER, BRIAN S.
 ; TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
 ; FILE REFERENCE: 059440/0141
 ; CURRENT APPLICATION NUMBER: US/10/051,307
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: 60/263,224
 ; PRIOR FILING DATE: 2001-01-23
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1598
 ; TYPE: DNA
 ; ORGANISM: Solanum tuberosum
 US-10-051-307-2

Query Match 86.3%; Score 1334.4; DB 14; Length 1598;

Best Local Similarity 93.8%; Pred. No. 5.1e-283;

Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;

Qy 1 ATCTTTGTTGTTGAAATAATTTGAAAGACCTTAGGACCAATCGACCTTGGGTGCAACAAT 60
 Db 49 ATCTTTGTTGTTGAAATAATTTGAAAGACCTTAGGACCAATCGACCTTGGGTGCAACAAT 108
 Qy 61 ATTGTTGTCCTCCAAATGTTGTTACAGGATTTACATCCTCCGGGTACTTTAAGTGCAC 120
 Db 109 ATTGTTGTCCTCCAAATGTTGTTACAGGATTTACATCCTCCGGGTACTTTAAGTGCAC 168
 Qy 121 TAGGACATTCACCATTTATTTGCGTGCATTTGATGCGTGGCATTTCCCTCCACTTG 180
 Db 169 TAGGACATTCACCATTTATTTGCGTGCATTTGATGCGTGGCATTTCCCTCCACTTG 228
 Qy 181 GATTAGTCCGGGCGAAAGTCAATCGGTATATTTAAATCCATCAACTAAAGAAATGTCACAG 240
 Db 229 GATTAGTCCGGGCGAAAGTCAATCGGTATATTTAAATCCATCAACTAAAGAAATGTCACAG 288
 Qy 241 AATCTAAGTTTGTAACTGGTCCGAGCGGTACTCGGCTAGGTGTTTGGGGTTTACCCC 300
 Db 289 AATCTAAGTTTGTAACTGGTCCGAGCGGTACTCGGCTAGGTGTTTGGGGTTTACCCC 348
 Qy 301 ACCGGTGCATCTCAGGACACCAACCAATCACCAGTCAATGACGCAACCTCTACACGAC 360
 Db 349 ACCGGTGCATCTCAGGACACCAACCAATCACCAGTCAATGACGCAACCTCTACACGAC 408
 Qy 361 CATCGAAGTTTACATCCAGTACGACCCCATATATAGTGCCTATCGTAGTGCCTTAGGGCGCAT 420
 Db 409 CACCGAAGTTTACATCCAGTACGACCCCATATATAGTGCCTATCGTAGTGCCTTAGGGCGCAT 468
 Qy 421 CAATGACCCACGTTTGGCTCGATCGAGAGTGGCCACCGCTATCGGGGTGATGCTG 480
 Db 469 CAATGACCCACGTTTGGCTCGATCGAGAGTGGCCACCGCTATCGGGGTGATGCTG 527
 Qy 481 CCACAGCGTGTATGACAGTGTGTTG-- --CGTACCTCGATAGTGGCAGCATTAAGTGAAGT 538
 Db 528 CCACAGCGTGTATGACAGTGTGTTGCGGCTACCTCGATAGTGGCAGCATTAAGTGAAGT 587
 Qy 539 CACAAAGCAAGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGCCCATGTTTGTGTAAT 598

Db 588 CACAAAGCCAGAGGAGGAGACCAAAAGAGATCTCAAGTAGCCCATGTTGTGAAAT 647
Qy 599 TTATATGTGGACAAATATTTTGTGACTTTATATATAGGATATGGCGCTTTTGGCAC 658
Db 648 TTATATGTGGACAAATATTTTGTGACTTTATATATAGGATATGGCGCTTTTGGCAC 707
Qy 659 TATGATATTAATCTATATATACATATCTTGTGACTTAATATATAACAAATAT 718
Db 708 TACGATATTAATCTATATATACATATCTTGTGACTTAATATATAACAAATAT 767
Qy 719 ATTACAATATATGTTGGTAAACGTTGAGTGGCCAAATGTATAAGAGCCGCTTAATAT 778
Db 768 ATTACAATATGTTGGTAAACGTTGAGTGGCCAAATGTATAAGAGCCGCTTAATAT 827
Qy 779 AATATATTTATGATATAGACTATAGTTTCAAGTGAACCTTTATTTGGTATACCTGGAC 838
Db 828 AATATATTTATGATATAGCTATAGTTTCAAGTGAACCTTTATTTGGTATACCTGGAC 887
Qy 839 ATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAATATATAAAGCAGCTATT 898
Db 888 ATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAATATATAAAGCAGCTATT 947
Qy 899 TTAATATTTTGTGGCCAAAGTTCTTGTGACTTATCTATGCCCCATTTTACTTTTAT 958
Db 948 TTAATATTTTGTGGCCAAAGTTCTTGTGACTTATCTATGCCCCATTTTACTTTTAT 1007
Qy 959 CGTTCTAGCCCTTCTAGGTAGCTGTTTGAACATATAAATCATATAAATGTAAGATTAATA 1018
Db 1008 CGTTCTAGCCCTTCTAGGTAGCTGTTTGAACATATAAATCATATAAATGTAAGATTAATA 1067
Qy 1019 TTAG---TTTTTTTTCATATTAATCTGATGATCATTTGTTAGATCAATGTGAATATAC 1075
Db 1068 TTAGTTTTTTTTTTCATATTAATCTGATGATCATTTGTTAGATCAATGTGAATATAC 1127
Qy 1076 AAATCATCTGATTTTAAATCATACATCTTCTGATGATGGAACGCTCATGGTATTC 1135
Db 1128 AAACCATCTGATTTTAAATCATACATCTTCTGATGATGGAACGCTCATGGTATTC 1186
Qy 1136 GTGCAAGTGTGATTTATTTAAGTCTGATGATGGAACGCTCATGGTATTC 1195
Db 1187 GTGCAAGTGTGATTTATTTAAGTCTGATGATGGAACGCTCATGGTATTC 1245
Qy 1196 CTATATAAAGAACCCCTATTTGATGCAAAAGTCAATAA--TATTTAATATCAATNCTTA 1253
Db 1246 CTATATAAAGAACCCCTATTTGATGCAAAAGTCAATAA--TATTTAATATCAATNCTTA 1305
Qy 1254 TTTATTTTACGATCGAGCATGATATCTTACTAATTAATAAATAATGGAAGGATTC 1313
Db 1306 TTTATTTTACGATCGAGCATGATATCTTACTAATTAATAAATAATGGAAGGATTC 1365
Qy 1314 ATGCAAGTCAATGATCTATCGTATCCCAATTTCCCTTAAAGTATGCTGCTT 1373
Db 1366 ATGCAAGTCAATGATCTATCGTATCCCAATTTAGGATACGTTAGTATGCTGCTT 1425
Qy 1374 TTAGAGAAACAGTGGATCATGATATTTTGTGATTTTCCCTTATCTCTTAAATATCTAT 1433
Db 1426 TTAGAGAAACAGTGGATCATGATCTATGATTTAGTATTTTCCCTTAAATATCTCTT 1485
Qy 1434 ATATACCTCTAAACCTAAATGATCTATAACCAACAAATATAAATAGTATCTTTAAAGA 1493
Db 1486 CTATCCCTCTTAAACCTAAATGATCTATAACCAACAAATATAAATAGTATCTTTAAAGA 1545
Qy 1494 AATTCAGATTTAAATGGAGGCAAAATAGTCTATGTTGAGTTGTTGCTTTC 1546
Db 1546 AATTCAGATTTAAATGGAGGCAAAATAGTCTATGTTGAGTTGTTGCTTTC 1598

RESULT 4

US-10-341-961A-371/c

; Sequence 371, Application US/10341961A

; Publication No. US20040006781A

; GENERAL INFORMATION:

; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Crasta, Oswald
; APPLICANT: Switsky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE
; FILE REFERENCE: BTI.67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; PRIOR APPLICATION NUMBER: 2003-01-14
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60361029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: Patent version 3.1
; SEQ ID NO 371
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-371

Query Match 18.8%; Score 291.2; DB 16; Length 510;
Best Local Similarity 78.1%; Pred. No. 6.8e-54;
Matches 350; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 ATCTTTGTTTGAATAAATTTGGAAGAAGACGTAGGACCAATGACCTTGGGTGCAACAAT 60
Db 448 ATCTTTGTTTGAATAAATTTGGAAGAAGACGTAGGACCAATGACCTTGGGTGCAACAAT 389
Qy 61 ATTTGTTGCTTCCAAATGTGTACAAGGATTTTACATCTCTCGGTTACTTTAAAGCTGAC 120
Db 388 ATTTGTTGCTTCCAAATGTGTACAAGGATTTTACATCTCTCGGTTACTTTAAAGCTGAC 329
Qy 121 TAGGACATTTACCATTTATTTTCCGTCGATTTGAATTTGATTTGATTTGATTTGATTTG 180
Db 328 CAGGCAATTTACCGTTTATTTGCTGTGATTTGATTTGATTTGATTTGATTTGATTTG 269
Qy 181 GATTAGTCCGGGCGAAAGTCTATCGGTATTTAAATCCATCAATCAATCAATCAATCAATCA 240
Db 268 GCTTAGTTGGCCAAAGACATAGGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 209
Qy 241 AATCTAAGTTTGAATCTGTCGAGCGGTACTCGGCTAGGTTGGTGGCGGTTTACCC 300
Db 208 AATCTAAGTTTGAATCTGTCGAGCGGTACTCGGCTAGGTTGGTGGCGGTTTACCC 149
Qy 301 ACCCGGTGCTAGTCCAGGACCAACCAATCAATCAATCAATCAATCAATCAATCAATCA 360
Db 148 ATCTTTTGAATCTGTCGAGCGGTACTCGGCTAGGTTGGTGGCGGTTTACCC 89
Qy 361 CATCAAGTTTACATCTAGTACGACCCCATATAGTGCATCTAGTCCCTTAGGCGCAT 420
Db 88 CATCAAGTTTGAATCTAGTACGACCCCATATAGTGCATCTAGTCCCTTAGGCGGCC 29
Qy 421 CAATGACCCAGTTTGGCTCGATCGAG 448
Db 28 AAAACCACTGCTGACCTCTCTCGAG 1

RESULT 5

US-05-938-842A-2118/c

; Sequence 2118, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 13.4%; Score 207.2; DB 9; Length 735;
Best Local Similarity 64.6%; Pred. No. 2.4e-35;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 43 GACCTTGGGTGCAACAATATTGTTGCTCTCCAAATGTTGGTACAGGATTTGTATCTCTC 102
Db 535 GACCGTTTCGTACACAGTATTGGTTCGTTGAATACAGTACACGGTGTGTCATCCAC 476

Qy 103 CGGTACTTTAAGCTGACTAGGACATTCACATTTATATTGCGTGCATTTGAATTCGCT 162
Db 475 CTGGGGCTCTCAACACGTTTGGACATTTGCGTTTATGTTCTGCGGTACATAGTATCCGAT 416

Qy 163 GGCATTTCCCTCCACTTGGATTAGTTCGGGGGAAAGTCATCGGTATATTAAATCCATCAA 222
Db 415 GGCAGTTC-----GAACTAGTTGGGCTAAACTCCNTAGGTATGTTAAATCCATCGA 365

Qy 223 CTAAAGAAATGTCGCCAAGAAATCTAAGTTGTTGAACTGCTCGAGGCGTACTCGGCTAGGG 282
Db 364 CAAGTGAGATATCGTAGAAGTCTAAGTTGTTGAATTTGGTTCAAGCGTACTCGAGCCAAAG 305

Qy 283 TGTGTTGGGTTTACCCACCGGTGCACTGCAGGACACCAATCCAGTATCGTATCG 342
Db 304 TGTGTTGGGTTGTTCCCGAGCCAGTACATTTGGATTCACCACTCGATCCACGTTGGC 245

Qy 343 ACGAACTCTACAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATACGTGCAATCG 402
Db 244 ATCGGCCACGACCTGAGGAGTCAAAGTTTACAATTTGGTCTACCCCAATCCGTGCCATTT 185

Qy 403 TAGTGCCCTTAGGCGCATATGACCCAGTTTGGCTCGATCGAGAGTTCGGCCACCGC 462
Db 184 TAGTGCCCGCGGACATCTAGCCTTCCATGATTTGGCCAGCATCTAGACGTGGGCCACCTC 125

Qy 463 CTATCGGGTCTGATGCTGCCAGAGCGGTGTATGACAGTGTGTTGGTACTCTCGATAGTGG 522
Db 124 C---AGGCTTGGCGAGCCACACGGTGTAACTACATTTGTTAGGATTTGGAATGTGG 68

Qy 523 CAGCATAGTGAAGTCAAAAGCAAGAAAGGAGAGAAACAAAGAGATCTCAAG 578
Db 67 CGGCTGTTGGTGGAGATGAGCAAAAGTGCAGAAAGTGCAGAAATATGAAAGTAGAGACCAAG 12

RESULT 6
US-09-938-842A-2118/c
; Sequence 2118, Application US/09938842A
; Publication No. US2004009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepis, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2118
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2118

Query Match 13.4%; Score 207.2; DB 11; Length 735;
Best Local Similarity 64.6%; Pred. No. 2.4e-35;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 43 GACCTTGGGTGCAACAATATTGTTGCTCTCCAAATGTTGGTACAGGATTTGTATCTCTC 102
Db 535 GACCGTTTCGTACACAGTATTGGTTCGTTGAATACAGTACACGGTGTGTCATCCAC 476

Qy 103 CGGTACTTTAAGCTGACTAGGACATTCACATTTATATTGCGTGCATTTGAATTCGCT 162
Db 475 CTGGGGCTCTCAACACGTTTGGACATTTGCGTTTATGTTCTGCGGTACATAGTATCCGAT 416

Qy 163 GGCATTTCCCTCCACTTGGATTAGTTCGGGGGAAAGTCATCGGTATATTAAATCCATCAA 222
Db 415 GGCAGTTC-----GAACTAGTTGGGCTAAACTCCNTAGGTATGTTAAATCCATCGA 365

Qy 223 CTAAAGAAATGTCGCCAAGAAATCTAAGTTGTTGAACTGCTCGAGGCGTACTCGGCTAGGG 282
Db 364 CAAGTGAGATATCGTAGAAGTCTAAGTTGTTGAATTTGGTTCAAGCGTACTCGAGCCAAAG 305

Qy 283 TGTGTTGGGTTTACCCACCGGTGCACTGCAGGACACCAATCCAGTATCGTATCG 342
Db 304 TGTGTTGGGTTGTTCCCGAGCCAGTACATTTGGATTCACCACTCGATCCACGTTGGC 245

Qy 343 ACGAACTCTACAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATACGTGCAATCG 402
Db 244 ATCGGCCACGACCTGAGGAGTCAAAGTTTACAATTTGGTCTACCCCAATCCGTGCCATTT 185

Qy 403 TAGTGCCCTTAGGCGCATATGACCCAGTTTGGCTCGATCGAGAGTTCGGCCACCGC 462
Db 184 TAGTGCCCGCGGACATCTAGCCTTCCATGATTTGGCCAGCATCTAGACGTGGGCCACCTC 125

Qy 463 CTATCGGGTCTGATGCTGCCAGAGCGGTGTATGACAGTGTGTTGGTACTCTCGATAGTGG 522
Db 124 C---AGGCTTGGCGAGCCACACGGTGTAACTACATTTGTTAGGATTTGGAATGTGG 68

Qy 523 CAGCATAGTGAAGTCAAAAGCAAGAAAGGAGAGAAACAAAGAGATCTCAAG 578
Db 67 CGGCTGTTGGTGGAGATGAGCAAAAGTGCAGAAAGTGCAGAAATATGAAAGTAGAGACCAAG 12

RESULT 7
US-09-770-445-334/c
; Sequence 334, Application US/09770445
; Patent No. US2002002381A1
; GENERAL INFORMATION:
; APPLICANT: Gorchach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja

; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurban, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; TITLE OF INVENTION: thaliana
 ; FILE REFERENCE: 202305 (PARA-012PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,445
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: US 60/178,472
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 334
 ; LENGTH: 950
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-445-334

Query Match 13.4%; Score 207.2; DB 9; Length 950;
 Best Local Similarity 64.6%; Pred. No. 2.8e-35;
 Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;
 QY 43 CACCTTGGGTGCAACAAATATTGTTGCTCTCCAAATGTGTACAGGATTGTTACATCCTC 102
 DB 543 GACCGTTCGTACACAGATTGTTGCTCTGAATACAGTACACGGGTTGTTGATCCAC 484
 QY 103 CGGTACTTTAAGTGTACTAGACATTCACATTTATATTGTCGGTGCATTTGAATGCGT 162
 DB 483 CTGGGGTCTCAACACGCTTTGGACATTTGCGTTTATGTTGCTGCGGTACATAGTATCCGAT 424
 QY 163 GGCATTTCCTCCACTTGGATTGCTCGGGGCAAGTTCATCGGTATATTAAATCCATCAA 222
 DB 423 GCGAGTTC-----GACATGTTGGGCTAAACTCCATAGGTATGTTAAATCCATCGA 373
 QY 223 CTAAGAAATATGCCCAAAATCTAAGTTGTTGAATCGTCCGAGGGGTACTCGGCTAGGG 282
 DB 372 CAAGTGAGATATCGTAGAAGTCTAAGTTGTTGAATGTTCAAAGCGTCTCAGCCAACG 313
 QY 283 TGTTTGGCGTTTACCCCAACCGGTGCATGTCAGGACACACACATCACAGTCAATGC 342
 DB 312 TGTTTGGCGTGTCCCAACCGTCAATGAGTCCACACTGCACTGCACTACCAAGTTGGC 253
 QY 343 ACGAACCTCTACAGACACCATCGAAGTTATCATCCAGTACGACCCCATATACGTGCGCATCG 402
 DB 252 ATCGGCCACGACCTGAGGAGTCAGATTAATGTTGCTTACCCCAATCCGTGCCATTT 193
 QY 403 TAGTGGCCCTAGGGGATCAATGACCCACGTTTGGCTCGATCGAGCGTGGGCCACCGC 462
 DB 192 TAGTGGCCCGCGGACATCTAGCTCCATGATTGGCCAGCATCTAGACGTGGGCCACCTC 133
 QY 463 CTATCGGGGTGATGCTGTCGCGACGCGTGTATGACAGTGTGTTGCGTACCTCGATAGTGG 522
 DB 132 C---AGGGCTTGGCGACGCCACACGCTGTACTATGTTTAGATTTGCAATGGG 76
 QY 523 CAGCATTAAGTGAAGTCAAAAAGCAAGAGGAGGAGAAAAACAAAGAAAGATCTCAAG 578
 DB 75 CGGCTGTTGGGTGGAGATGAGCAAAAGTGGGAAAAATATGAAAGTAGAGACCAAG 20

RESULT 8
 US-10-424-599-103619/c
 ; Sequence 103619, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 103619
 ; LENGTH: 909
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_64586C.1
 US-10-424-599-103619
 Query Match 11.8%; Score 182.4; DB 13; Length 909;
 Best Local Similarity 61.4%; Pred. No. 7.8e-30;
 Matches 329; Conservative 0; Mismatches 201; Indels 6; Gaps 2;
 QY 1 ATCTTTGTTGAAAAAATTTGAAAAAGACGTAGGACACATGACCTTGGGTGCAACAAT 60
 DB 628 ACCTTTGCTTGAAGATCTGGATTAATCAGTGGGCCACAGCTACCGGAATTCACACAGT 569
 QY 61 ATGTGTGCTCTCAAAATGTGTGACAAAGATTGTTACATCTCTCGGGTACTTTAAGCTGAC 120
 DB 568 ACTGTCGCTTTTGAAGACAGTGCAGAGGTTGTTGCAACCTCTTGTAGTCTTTAGCTCAC 509
 QY 121 TAGGACATTCACATTTATATTGTCGGTGCATTGAATTCGCTGGCAATTCCTCCACTTG 180
 DB 508 TAGGCACTGTCCGTTAATGTCGGCAGTGC---GCTTATGCCACGTGTGCATCCATTCG 452
 QY 181 GATTAGTCCGGGCGAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGTCACAGA 240
 DB 451 ---AGTTGGACTAAAGTCCATGGGCAGCTTAAACCGTCGACGAGGAGATGTCGAAGA 395
 QY 241 RATCTAAGTCTTGAAGTGTTCGAGGCGTACTCGGCTAGGCTGTTGGCGGTTTACCCC 300
 DB 394 AGTCAAAATTTGTTAAACCCGTTTCAAGGCGGTATTGAGCCAGGCTGTTGGAGGCGCACCGT 335
 QY 301 ACCCGGTGCTGTCAGGACACACACATCAACAGTCAATGACAGAACCTTACAGCAC 360
 DB 334 AAGCTTTCAGTTCAGGACACACCCCGGAGTCAACCGTCTGTCATCCACCGGCGCCGAAC 275
 QY 361 CATCGAAGTACATTCAGTACACCCCATATACGTGCCATCGTAGTGCCTTAGGCGCAT 420
 DB 274 CGTGAAGTTTCAGCGCGTTTCGGGCCCAACCGCGGCGCCCTTTCGTTCTGTCAGGCACT 215
 QY 421 CAATGACCCACGTTTGGCTCGATCGAGAGCTGCGGCCACCGCTATCGGGGTGATGCTG 480
 DB 214 CCACGGACCATGACTGGCCCGGTTTAATTGACGCCACCGCCCAAGGACAGACGACGAG 155
 QY 481 CCCAGACGTTATGGAAGTGTGTTGCGTACCTCGATGTTGGCAGCAGATAAGTGAAG 536
 DB 154 CCCAGACGTTATGTCATCGGTTTGTGATTTCAAACTTGCAGCATATGCGGAA 99

RESULT 9
 US-10-636-396-4/c
 ; Sequence 4, Application US/10636396
 ; Publication No. US20040073971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,396
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01

```

; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-4

Query Match      11.7%; Score 180.6; DB 12; Length 875;
Best Local Similarity 60.9%; Pred. No. 1.9e-29;
Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTTGAAGAAATTTGAAGAACGCTAGGACACATGGACCTTGGGTGCAACAAT 60
   |||||
Db 577 ATCTGGCTTGAAGAAACCTTGATTAATCAGTTGGTCCACAATTTCCAGAGTTGCAACAAT 518

QY 61 ATTGTTGTCCTCCAAATGTTGTAACAGGATTTTACATCCTCCGGGTACTTTAAGCTGAC 120
   |||||
Db 517 ACTGATCAGTTTGTACAGGTTGCAAGGTTATTGCAACCCGCGAGGAGCCCGTAATCAC 458

QY 121 TAGGACATTCACCAATTTATTTGCCGTGCAATTTGCGTGGGATTTCCCTCCACTTG 180
   |||||
Db 457 CAGGACACTGGCCATTTGATATCCGCAATGATGATACCCCGGTGCAACCC-----AT 404

QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCAATCAATCAATCAATCAATCAAT 240
   |||||
Db 403 TAGAATTCGGTCTAAACACCAATCGGCACATTTGAATCCGTCACACAGAGAAATGTCAAGA 344

QY 241 AATCTAAGTTGTTGAATCTGGTCCGAGGCGTACTCGGTAGGTTGTTGGGGTTTACCCC 300
   |||||
Db 343 AATCAAGATTTGTTGAATCTGGTTCAAAGCGTACTCGGCCAATGTGTTGGGTGGGTACCAT 284

QY 301 ACCCGGTGCATCGCAGGACACCAATCACCAGTCAATCAGGACCTTACACGAC 360
   |||||
Db 283 AGTTTGGCATTTGGAGAGACCGTTTGCATCACCCTCTGACACCTCGCTCGCCAGAAC 224

QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATTCGTCAGTCCCTTAGCGCAT 420
   |||||
Db 223 CATCAAGTTGCAATTTGTTGGGGCCATATACGGCTCTGTCAGTCCAGCTGCGACGG 164

QY 421 CAATGACCCACGTTTGGCTCGATCGAGACGTCGCGCCACCGCTATCGGGTTCATGCTG 480
   |||||
Db 163 TTAAAGACACGTTTGGCTCGATTAAGTTGTCGGCCCGCCACC---AGGCACCCGACCCAG 107

QY 481 CCCAGACGCTGTATGACAGCTTTGTCGTACCTCGATAGTGCAGCATTAAGTAAAGTCA 540
   |||||
Db 106 CCCAAACGCTGTATGACAGCTTTGTCGAATAGTGAACACGCGCTGCATTGGTATAGTAA 47

QY 541 CAAAA 545
   |||
Db 46 AAAGA 42

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```

RESULT 10
US-10-636-026-4/c
; Sequence 4, Application US/10636026
; Publication No. US20040111761A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Duval, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,026
; CURRENT FILING DATE: 2003-08-07
; PRIOR FILING DATE: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904

```

```

; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-026-4

Query Match      11.7%; Score 180.6; DB 17; Length 875;
Best Local Similarity 60.9%; Pred. No. 1.9e-29;
Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTTGAAGAAATTTGAAGAACGCTAGGACACATGGACCTTGGGTGCAACAAT 60
   |||||
Db 577 ATCTGGCTTGAAGAAACCTTGATTAATCAGTTGGTCCACAATTTCCAGAGTTGCAACAAT 518

QY 61 ATTGTTGTCCTCCAAATGTTGTAACAGGATTTTACATCCTCCGGGTACTTTAAGCTGAC 120
   |||||
Db 517 ACTGATCAGTTTGTACAGGTTGCAAGGTTATTGCAACCCGCGAGGAGCCCGTAATCAC 458

QY 121 TAGGACATTCACCAATTTATTTGCCGTGCAATTTGCGTGGGATTTCCCTCCACTTG 180
   |||||
Db 457 CAGGACACTGGCCATTTGATATCCGCAATGATGATACCCCGGTGCAACCC-----AT 404

QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCAATCAATCAATCAATCAATCAAT 240
   |||||
Db 403 TAGAATTCGGTCTAAACACCAATCGGCACATTTGAATCCGTCACACAGAGAAATGTCAAGA 344

QY 241 AATCTAAGTTGTTGAATCTGGTCCGAGGCGTACTCGGTAGGTTGTTGGGGTTTACCCC 300
   |||||
Db 343 AATCAAGATTTGTTGAATCTGGTTCAAAGCGTACTCGGCCAATGTGTTGGGTGGGTACCAT 284

QY 301 ACCCGGTGCATCGCAGGACACCAATCACCAGTCAATCAGGACCTTACACGAC 360
   |||||
Db 283 AGTTTGGCATTTGGAGAGACCGTTTGCATCACCCTCTGACACCTCGCTCGCCAGAAC 224

QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATTCGTCAGTCCCTTAGCGCAT 420
   |||||
Db 223 CATCAAGTTGCAATTTGTTGGGGCCATATACGGCTCTGTCAGTCCAGCTGCGACGG 164

QY 421 CAATGACCCACGTTTGGCTCGATCGAGACGTCGCGCCACCGCTATCGGGTTCATGCTG 480
   |||||
Db 163 TTAAAGACACGTTTGGCTCGATTAAGTTGTCGGCCCGCCACC---AGGCACCCGACCCAG 107

QY 481 CCCAGACGCTGTATGACAGCTTTGTCGTACCTCGATAGTGCAGCATTAAGTAAAGTCA 540
   |||||
Db 106 CCCAAACGCTGTATGACAGCTTTGTCGAATAGTGAACACGCGCTGCATTGGTATAGTAA 47

QY 541 CAAAA 545
   |||
Db 46 AAAGA 42

```

```

RESULT 11
US-10-424-599-36321/c
; Sequence 36321, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36321
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Glycine max

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/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(1956)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_132800C.1
US-10-424-599-36321

Query Match      11.1%; Score 171.6; DB 13; Length 1956;
Best Local Similarity 59.8%; Pred. No. 2.8e-27;
Matches 329; Conservative 0; Mismatches 209; Indels 12; Gaps 2;

QY 39 CATGACCTTGGTGCACAAATATTGTTGCTCTCAAAATGGTGACAGGATTTGTCAT 98
Db 1290 CTTGCCCAATGGTGCAGCACTACTCATTCGTTCTTAAACACAGATGTCAGGGGTTGTCAT 1231
QY 99 CTTCCGGGTACTTTAAGCTGACTAGGACATTCACCATTTATATTGCGGTGCAATGAATT 158
Db 1230 CCCCAGGTGCCCTTAATGGCCCGGGCACTGCCCATTTGATATCAGCGCTCAACTGATT 1171
QY 159 GGTGGCAATTCCTCCCACTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAATCCA 218
Db 1170 TTGTGACACCCACCG-----TTTAGAGGGTAGAAGTCCATCGGAATGTTGAACCG 1120
QY 219 TCAACTAAAGAAATGCTCCGAAATCTAAGTTGTTGAACTGGTCCGAGGGTACTCGCT 278
Db 1119 TCACCAAGAGATGCTGAGAAATCTGTTGCAAAATGGTTCAACGGGAATTCGCA 1060
QY 279 AGGTGTTTGGCGGTTTACCCACCCCGGTGCACTGCAGGACACCAACATCACCAAGTC 338
Db 1059 AGTGTGTTGGAGGAGACCCCGGCTTGGCAATTTAGGCGCGCGTCTCCGTT 1000
QY 339 ATGCAAGAACCTTACCAAGACCACTGAAATGATCATCGAGTACGACCCCATATAGTGCC 398
Db 999 TGGCAGCGCGCGCGCGCTCCCAATCAAAAGTTGACCGGTGCGGGCCCATATACGGGCC 940
QY 399 ATCGTAGTCCCTAGGCGGCATCAATGACCCACGTTTGGCTCGATCGAGACGTCGSCCA 459
Db 939 ATGCAAGTCCCGGTTTACCCAGAGTTTCAAGTTTGGCCACGGTTCACAGCGCGCT 890
QY 459 CGGCTATCGGGTGCATGTCGCCAGACGGTGTATGGAAGTGTGCGTATCTGATA 518
Db 879 CCACC---CGGACTCGCGCGCGCCACACCGTGTAGGGGCAATTTGTGACGATCTCGAAG 823
QY 519 GTGCAGCATAGTGAAGTACAAAAGCAAGAGGAGGAGGAGAAACAAAAGAGTCTCAG 578
Db 822 TTTCGACATGATTTGTTGCCAAGGTAAGGCCAACGTTAGCAGAGCAGTGCACAG 763
QY 579 TAGCCCAATGT 588
Db 762 TAAACCAATTT 753

RESULT 12
US-10-259-165-389/c
; Sequence 389, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCES: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
```

```
/ CURRENT FILING DATE: 2002-09-26
/ PRIOR APPLICATION NUMBER: US 60/370,620
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/368,327
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26
/ NUMBER OF SEQ ID NOS: 782
/ SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
/ SEQ ID NO 389
/ LENGTH: 717
/ TYPE: DNA
/ ORGANISM: Oryza sativa
US-10-259-165-389

Query Match      10.1%; Score 155.8; DB 15; Length 717;
Best Local Similarity 57.9%; Pred. No. 4.8e-24;
Matches 297; Conservative 0; Mismatches 212; Indels 4; Gaps 1;

QY 50 GGTGCAACAATATTGTTGCTCTCCAAATGTGTACAAAGGATTTTACATCTCTCCGGGTAC 109
Db 541 GGTGCAAGCACTACTGTCCTGCTTGAACACCGTGCACGGTGTGTCACCGCGCGGGCGC 482
QY 110 TTTAAGCTGACTAGGACATTCACCATTTATATTTCGCGTGCATTTGAATTGG----TGGC 165
Db 481 CTTCAAGTCTGCTCGGGCACTGCCCCCGCCACCGTCCGCTCGCACCGCGCGCGCTTGGC 422
QY 166 ATTTCTCTCACTTGGATTAGTCGGGGGAAAGTCACTCGGTATATTAATTCATCAACTA 225
Db 421 GCACCGCGCGCTGCGCGGGGGGAGGAGTCCATGCGCACGTTGAATTCGTGATGA 362
QY 226 AAGAAATGTCGAGAAATCTAAGTTGTTGAATCTGATCGAGCGGTACTCGGCTAGGGTGT 285
Db 361 GGGAGATGTGCAAGAAAGTCGAGGTTGCTGAACTGTTTCAAGCGCAACTCCGCGCGGTGT 302
QY 286 TTGGCGGTTTACCCACCCCGGTGCACTGCAGGACACCAACCAATCCACGATCATGACG 345
Db 301 TGGGCGGTGTCCTGCTGACCGCGCACCGCAGACCGCGCGCGGTGCGCGCTGCGCAC 242
QY 346 AACCTCTACCAAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATAGTCCCATCGTAG 405
Db 241 GCCCGTTCGCGTGCCTGCGTGAAGTTCGAGCGCGTGCAGCGCCACACGCGCGCGCTCG 182
QY 406 TCGCCCTTAGGCGCATCAATGACCCACGTTTGGCTCGATTCGAGAGCTCGGCAACGCGCTA 465
Db 181 TCCCGCGCGGACGTCGATCACCACACTGCTGCCCGGGTCCAGTGTGTCGCCCGCGCGG 122
QY 466 TCGGGGTGATGCTGCTGCCAGACGGTGTATGAGACAGTTTGTTCGTACCTCGATAGTGGCAG 525
Db 121 ACGGCACGCTGCCGCCACACGCGTGATCTGGCACTTGTGTTGTTGTTGTTGTTGTTGTTG 62
QY 526 CATAAGTGAAGTCAAAAGCAAGAGGAGA 558
Db 61 CGTTCCGCGCGCGCGGAGGAGGAGAGGGA 29

RESULT 13
US-10-259-165-41/c
; Sequence 41, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
```



```

; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
;
; FILE REFERENCE: 70030-NP
;
; CURRENT APPLICATION NUMBER: US/10/259,165
;
; CURRENT FILING DATE: 2002-09-26
;
; PRIOR APPLICATION NUMBER: US 60/370,620
;
; PRIOR FILING DATE: 2002-04-04
;
; PRIOR APPLICATION NUMBER: US 60/368,327
;
; PRIOR FILING DATE: 2002-03-27
;
; PRIOR APPLICATION NUMBER: US 60/325,277
;
; PRIOR FILING DATE: 2001-09-26
;
; NUMBER OF SEQ ID NOS: 782
;
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
;
; SEQ ID NO 41
;
; LENGTH: 720
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
;
; US-10-259-165-41

```

Query Match	10.1%;	Score 155.8;	DB 15;	Length 720;	
Best Local Similarity	57.9%;	Pred. No. 4.9e-24;			
Matches 297;	Conservative	0;	Mismatches 212;	Indels 4;	Gaps 1;
Qy	50	GGTSCAACAAATATTGTTGCTCTCCAAATGCGTCAAGAGATTGTATCATCTCCGGGTAC	109		
Db	541	GGTGCACAGTACTGGTCTCTGCTTGAACACCGTGCACGCGTGTGTGACCCGCGGGCGC	482		
Qy	110	TTTAAAGGTGACTAGGACCAATTCACCAATTTATATTTGCCGTGCATTGCAATTTGCG----	165		
Db	481	CCTCAGCTCGCTCGGGCACTGCCCGCCACGCTCGCGCTCGCACGCGCGCGCGCTTGCC	422		
Qy	166	ATTTCCCTCCACTTGGAATTAGTCGGGGGGAAGTATCATCGGTATATTAAATCCATCACTA	225		
Db	421	GCACCCGGCGCGTTCGCGCGGGGAGAGAAAGTCCATGGGCACGTTGGAATCCGTGCATGA	362		
Qy	226	AAGAAATGTCGCCAGAAATCTAAAGTTGTGAACTGGTCCGAGCGCTACTCGGTAGGCGT	285		
Db	361	GGGAGATGTCGAAGAAGTCTGAGGTGCTGAATCTGGTTCAGCGCGAACTTCGCCACGCT	302		
Qy	286	TTGCGCGGTTTACCCACCACCGGTGCACCTCGAGGACACCAACCAATCACCACTCATGCA	345		
Db	301	TGGCGCGGTGCCGCTAGCGCGCACCGCAGCACGCGCGCGAGTCGCGCGCTCTGGCACC	242		
Qy	346	AACCTCTACGACGACCATCGAAGTTTACATCCAGTACGACCCCATATAGTGCATCGTAG	405		
Db	241	GCCCGTTGCCGCTGCGGTCGAAGCTGCAAGCCGCTGCGCGCCACACGCGCGCCGCGCTG	182		
Qy	406	TGCCCTTAGGGCGCATCAATGACCAACCGTTTGGCCCTCGATCGAGACGTCGGCGCACCGCCTA	465		
Db	181	TGCCGCGCGGACGTCGATCAACCACTGCTGCCCGGGTCAAGCTGCTGCCCGCGCGCGG	122		
Qy	466	TCGGGGTTCGATGCTGCCACAGCGGTGTATGGAACAGTTGTTCGCTACCTCGATAGTGGCAG	525		
Db	121	ACGGCACGGCTGCCGCCCCACACGCGTGATCTGSCACTTGTGTGATGTATGTAACGTGGCGG	62		
Qy	526	CATTAAGTGAAGTCAAAAACGAAAGGGAGA	558		
Db	61	CGTTCGCGCGCGCGGAGGAGGAGGAGGAGGA	29		

RESULT 14
US-10-437-963-86607/c
; Sequence 86607, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharev, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
;
; SEQ ID NO 86607
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85631C.1
; US-10-437-963-86607

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Query Match	9.9%	Score 153.6	DB 17	Length 1006
Best Local Similarity	57.6%	Pred. No. 1.8e-23		
Matches	295	Conservative 0	Mismatches 214	Indels 3
	Gaps			
QY	50	GGTGCAACAATATTGTTGCTCTCCAAATGTTGTTACAAAGATTGTATACATCTCCGGGTAC	109	
Db	584	GGTGCAGAGTACTGGTCTCTGCTTGAACCGTGCA CGGTGTTGTGACCCGCCGGGGCGC	525	
QY	110	TTTAAGCTGACTAGGACATTCACCATTTATATTTGGCGTGCAATTGAATGGC---TGGCA	166	
Db	524	CCTCAGCTCGCTCGGGCACTGCCCGGCCACGTCCTCGCACGCGCGCGCCCTTGCC	465	
QY	167	TTTCCCTCCACTTGGAATTAGTCGGGGGGAAGTATCGGTATATTAATTCATCAACTAA	226	
Db	464	GCACCCGGCGCGCTCGCGGGCGGGAGGAAGTCCATGGGCAGTTGAATCCGTGCATGAG	405	
QY	227	AGAAATGTCACAGAAATCTAAGTTGTTGAATCGGTGTCGAGCGCTACTCGGTAGGGTGT	286	
Db	404	GGAGATGTCGAAGAAGTCGAGGTTGCTGAACTGTTTTCAGCGGAACTCTCGGCAGGTGT	345	
QY	287	TGGCGGTTTACCCACCCCGGTGCACTGCAGGACACCAACCAATCAACGATCATSCAGA	346	
Db	344	GGCGGCTGCCGTAGCGCGCGCACCGCAGCACGCGCGCGAGTCGCCCGCTGSCACCG	285	
QY	347	ACTCTTACCAGCACCATCGAAGTTTACATCCAGTAGACCCCATATATCGTGCATCGTAGT	406	
Db	284	CCCGTTGCGGTGCGCTCGAAGCTGCAGCCGCTGCGCGCCACACGCGCCCGCCGTCGT	225	
QY	407	GCCTTAGCGGCATCAATGACCCAGCTTTGGCTTCGATCGAGACGTCGCGCACCCGCTAT	466	
Db	224	GC CGGCGCGGACGTCGATCACCCACTGCTGCCCGGGTCCAGCTGCTGCCCGCCGCGGA	165	
QY	467	CGGGTTCGATGTCGCCACAGCGGTGATGGACAGTTGTTGCGTACCTCGATAGTGGCAGC	526	
Db	164	CGGCACGCGCTGCCGCCACACGGTGATCTGGCACCTTTGTTGGTGATGCTGAACGTGGCGCG	105	
QY	527	ATAAGTGAAGTCAACAAGCAAGAGCGAGA	558	
Db	104	GTTCGCGCGCGCGGAGGAGGAGGAGGGA	73	

RESULT 15
US-10-424-599-7736/c
; Sequence 7736, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7736
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Glycine max

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 05:06:40 ; Search time 3634.85 Seconds
(without alignments)
12701.209 Million cell updates/sec

Title: US-10-051-307-3

Perfect score: 1546

Sequence: 1 atcttctgttgaaaaaattg.....tggtgaagtgggtgtcttc 1546

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
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13: gb_est4:*
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15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	505.2	32.7	899	14	CK252883 EST736520
C 2	505.2	32.7	1004	14	CK248798 EST73435
C 3	502	32.5	988	14	CK246326 EST729963
C 4	500.2	32.4	888	14	CK278032 EST724110

C 5	499.6	32.3	853	14	CK271811
C 6	499.2	32.3	899	14	CK252271
C 7	495.8	32.1	739	12	BI176339
C 8	490.2	31.7	649	9	AW039873
C 9	487.2	31.5	583	12	BI432833
C 10	486	31.4	622	10	BF053678
C 11	485.2	31.4	639	12	BGI30690
C 12	483	31.2	667	12	BI922472
C 13	480.8	31.1	585	9	AW031249
C 14	474.6	30.7	923	14	CK273930
C 15	474.4	30.7	593	9	AW032915
C 16	472.2	30.5	777	12	BM407898
C 17	471.4	30.5	651	10	AW218785
C 18	469.4	30.4	586	9	AW033588
C 19	469.4	30.4	649	10	AW222204
C 20	469.4	30.4	652	12	BI921170
C 21	469.4	30.4	669	12	BI921735
C 22	469.4	30.4	782	12	BM410787
C 23	467.2	30.2	944	14	CK271145
C 24	466.2	30.2	598	14	CA514039
C 25	462.8	29.9	936	14	CK277819
C 26	461.2	29.8	916	14	CK279273
C 27	461	29.8	638	12	BI434454
C 28	460.4	29.8	757	12	BI434095
C 29	460.4	29.8	657	10	AW223507
C 30	457.8	29.6	660	12	BM403979
C 31	457.8	29.6	776	12	BGI23660
C 32	457.2	29.6	575	12	BI421330
C 33	456.2	29.5	574	10	AW441774
C 34	455.4	29.5	604	12	BI423179
C 35	455.4	29.5	637	12	BI921311
C 36	455.4	29.5	719	12	BI422260
C 37	455.4	29.5	720	12	BI921826
C 38	455.4	29.5	807	12	BI421946
C 39	454.6	29.4	574	10	AW223623
C 40	454.4	29.4	626	9	AW033829
C 41	453.8	29.4	629	10	BE432710
C 42	453.8	29.4	635	12	BM403950
C 43	453.4	29.3	682	10	AW223970
C 44	453.4	29.3	710	9	AW035171
C 45	453.2	29.3	573	9	AW032317

ALIGNMENTS

RESULT 1
LOCUS CK252883/c 899 bp mRNA linear EST 12-DEC-2003
DEFINITION EST736520 potato callus cdna library, normalized and full-length
Solanum tuberosum cdna clone POC0086 5' end, mRNA sequence.
ACCESSION CK252883
VERSION CK252883.1 GI:39807285
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (Bases 1 to 899)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTC ACA CTA TAG.

FEATURES
source

Location/Qualifiers
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/organism="Solanum tuberosum"
/mol_type="mRNA"

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 /clone_lib="potato callus cDNA library, normalized and full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 32.7%; Score 505.2; DB 14; Length 899;
 Best Local Similarity 89.6%; Pred. No. 5.7e-94;
 Matches 543; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 60
 Db 608 ATCTTTGTTGAAAAAATCTAGACAAATCAGTAGGACACACATGGACCTTGGTGCAACAAT 549

QY 61 ATTGTTGTCCTCCAAATGTGTCAAGGATTTTACATCTCTCCGGGTACTTTAAGCTGAC 120
 Db 548 ATTGTTGTCCTCCGAACTGTGTCAAGGATTTTACATCTCTCCGGGTACTTTAAGCTGAC 489

QY 121 TAGGACATTCACATTTATTTGCGGTGCAATGAATGCGTGCAATTTCCCTCCACTTG 180
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QY 181 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATCAATGAAGATGCCCAGA 240
 Db 428 GATTGTTGGGCGAAAGTCAATCGGTATATTTAAATCCATCAATCAATGAAGATGCCCAGA 369

QY 241 AATCTAAGTTTGAATGTTGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 300
 Db 368 AATCTAAGTTTGAATGTTGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 309

QY 301 ACCGGGTGCTGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
 Db 308 ACCGGGTGCTGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 249

QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCATCGTGTAGTCCCTCCACTTG 420
 Db 248 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCATCGTGTAGTCCCTCCACTTG 189

QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTGGGCCACGCCCTATCGGGGTGATGCTG 480
 Db 188 TGATAACCCAGTTTGGCTCGATCGAGAGCTGGGCCACGCCCTATCGGGGTGATGCTG 129

QY 481 CCCAGAGCTGTATGGACAGTTGTTGGTACCTCGATAGTGGGACATAGTGAAGTCA 540
 Db 128 CCCAGAGCTGTATGGACAGTTGTTGGTACCTCGATAGTGGGACATAGTGAAGTCA 69

QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTTGTGAATTT 600
 Db 68 CAAAGCAAGAGGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTTGTGAATTT 9

QY 601 ATATGT 606
 Db 8 ATTTT 3

RESULT 2
 CK248798/c
 LOCUS
 DEFINITION EST732435 potato callus cDNA library, normalized and full-length
 Solanum tuberosum cDNA clone POCB364 5' end, mRNA sequence.
 CK248798
 ACCESSION
 VERSION CK248798.1 GI:39799290
 KEYWORDS
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 1004)
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
 Generation of ESTs from potato callus tissue
 Unpublished (2003)
 JOURNAL
 COMMENT
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
 1..1004
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POCB364"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 32.7%; Score 505.2; DB 14; Length 1004;
 Best Local Similarity 89.6%; Pred. No. 5.5e-94;
 Matches 543; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAGACGTAGGACACACATGGACCTTGGTGCAACAAT 60
 Db 607 ATCTTTGTTGAAAAAATCTAGACAAATCAGTAGGACACACATGGACCTTGGTGCAACAAT 548

QY 61 ATTGTTGTCCTCCAAATGTGTGACAGGATTTTACATCTCTCCGGGTACTTTAAGCTGAC 120
 Db 547 ATTGTTGTCCTCCGAACTGTGTGACAGGATTTTACATCTCTCCGGGTACTTTAAGCTGAC 488

QY 121 TAGGACATTCACATTTATTTGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 180
 Db 487 TAGGACATTCACATTTATTTAGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 428

QY 181 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATGAAGATGCCCAGA 240
 Db 427 GATTAGTCGGGGCGGAAAGTCAATCGGTATATTTAAATCCATCAATGAAGATGCCCAGA 368

QY 241 AATCTAAGTTTGTGAATGTTGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 300
 Db 367 AATCTAAGTTTGTGAATGTTGCGGTGCAATGAATGCGGTGCAATTTCCCTCCACTTG 308

QY 301 ACCGGGTGCTGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
 Db 307 ACCGGGTGCTGAGGACACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 248

QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCATCGTGTAGTCCCTCCACTTG 420
 Db 247 CATCGAAGTTACATCCAGTACGACCCCATATAGTCCATCGTGTAGTCCCTCCACTTG 188

QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTGGGCCACGCCCTATCGGGGTGATGCTG 480
 Db 187 TGATAACCCAGTTTGGCTCGATCGAGAGCTGGGCCACGCCCTATCGGGGTGATGCTG 128

QY 481 CCCAGAGCTGTATGGACAGTTGTTGGTACCTCGATAGTGGGACATAGTGAAGTCA 540
 Db 127 CCCAGAGCTGTATGGACAGTTGTTGGTACCTCGATAGTGGGACATAGTGAAGTCA 68

QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTTGTGAATTT 600
 Db 67 CAAAGCAAGAGGAGGAGGAGAAACAAAGAGAGATCTCAAGTAGGCCCATGTTTGTGAATTT 8

QY 601 ATATGT 606
 Db 1 ATTTT 1

Db	7	ATTTT 2	
RESULT 3			
CK246326/c			
LOCUS	EST729963	potato callus cDNA library, normalized and full-length	EST 12-DEC-2003
DEFINITION	Solanum tuberosum cDNA clone POCAL08 5' end, mRNA sequence.		
ACCESSION	CK246326		
VERSION	CK246326.1	GI:39793747	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.		
TITLE	Generation of ESTs from potato callus tissue		
JOURNAL	Unpublished (2003)		
COMMENT	Other ESTs: EST729964 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.		
FEATURES			
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		/clone="POCAL08"	
		/tissue_type="callus"	
		/lab_host="DH10B-Tona"	
		/clone_lib="potato callus cDNA library, normalized and full-length"	
		/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."	
ORIGIN			
	Query Match	32.5%;	Score 502; DB 14; Length 988;
	Best Local Similarity	90.0%;	Pred. No. 2.5e-93;
	Matches 538; Conservative	0;	Mismatches 60; Indels 0; Gaps 0;
Qy	1	ATCTTTGTTTGAATAAATTTGGAAGAACGTAGGACCATGGACCTTTGGGTGCAACAAT	60
Db	598	ATCTTTGTTTGAATAAATCTAGACAAATCAGTAGGACCATGGACCTTTGGGTGCAACAAT	539
Qy	61	ATTGTTGCTCCCAATGTGTACAGGATTGTTACATCTCTCCGGTACTTTAAGCTGAC	120
Db	538	ATTGTTGCTCTCCGAACGTGTACAGGATTGTTACATCTCTCCAGTACCTAAGTGAAC	479
Qy	121	TAGGACATTCACCAATTTATTTGCGGTGCAATTAATTCGCTGGCATTTCCCTCCACTTG	180
Db	478	CAGGACATTCACCAATTTATTTAGCGGTGCAATTAATTCGCTGGCATTTCCCTCCACTAG	419
Qy	181	GATTAGTCGGGGGGAAGTCATCGGTATATTAAATTCATCACTAAAGAAATGTCGAGA	240
Db	418	GATTGTTGGGGGAAAAGTCATCGGAATATTAAATTCATCGCACTAAAGAAATGTCGAGA	359
Qy	241	ATCTAAGTTGTTGAACCTGTCGGAGCGGTACTCGGCTAGGGTGTTCGCGGTTTACCCC	300
Db	358	AATCTAGGTTGCTGAACCTGTCAGGCGGTATTTCAGCCAGGGTGTTCGCGGTTTACCCC	299
Qy	301	ACCCGGTGCACCTGCAGGACACCAATCACTACAGTATGACGCAACCTCTTACAGCAC	360
Db	298	ACCCGGTGCACCTGCAGGACACCAATCACTACAGTATGACGCAACCTCTTACAGCAC	239
Qy	361	CATCGAAGTTAGTCAGCTAGACCCCATATACGTCGCATCGTAGTGCCTTAGGCGCAT	420

238	CATCAAAAGTTGCAATTAGTAGACCCCATATACGTGCATCTTAGTGCCTCGCGCAT	179
RESULT 4		
CK278032/c		
LOCUS	EST724110	potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE351 5' end, mRNA sequence.
DEFINITION		
ACCESSION	CK278032	
VERSION	CK278032.1	GI:39835010
KEYWORDS	EST.	
SOURCE	Solanum tuberosum (potato)	
ORGANISM	Solanum tuberosum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.	
AUTHORS	Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.	
TITLE	Generation of ESTs from abiotic stressed potato tissue	
JOURNAL	Unpublished (2003)	
COMMENT	Other ESTs: EST724111 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.	
FEATURES		
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		/db_xref="taxon:4113"
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		/lab_host="DH10B-Tona"
		/clone_lib="potato abiotic stress cDNA library"
		/note="Vector: pCMVSPORT6.1; site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."
ORIGIN		

ORIGIN

Db	238	CATCAAAAGTTGCAATTAGTACGACCCCATATAGTGCCATCTTTAGTGCCTCCGGCGCAT	179
Qy	421	CAATGACCCACGCTTTGGCCCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATGCTG	480
Db	178	TGATAACCCATGCTGCGCTCGATCGAGAGCTGGCCACCGCTATCGGGGTGATGCTG	119
Qy	481	CCGACAGCGGTGATGACAGCTTTTCGCTACCTCGATAGTGGCAGCATTAAGTGAAGTCA	540
Db	118	CCGACAGCGGTGATGACAGCTTTTCGCTACCTCGATAGTGGCAGCATTAAGTGAAGTCA	59
Qy	541	CAAAAGCAAGAGGAGAAACAAAGAGATCTCAAGTAGCCATCTTTGTTGGAAT	598
Db	58	CAAAAGCAAGAGGAGAAACAAAGAGATCTCAAGTAGCCATCTTTGTTGGAAT	1

RESULT 4			
CK278032/c			
LOCUS	CK278032	888 bp	mRNA linear EST 12-DEC-2003
DEFINITION	EST724110 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAE351 5' end, mRNA sequence.		
ACCESSION	CK278032		
VERSION	CK278032.1	GI:39835010	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.		
AUTHORS	Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.		
TITLE	Generation of ESTs from abiotic stressed potato tissue		
JOURNAL	Unpublished (2003)		
COMMENT	Other ESTs: EST724111 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.		


```

||||| 54 CAAAAGCAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGGT 1
|||||
||||| 589 bp mRNA linear EST 12-DEC-2003
CK252271 potato callus cDNA library, normalized and full-length
EST735908 Solanum tuberosum cDNA clone POC8787 5' end, mRNA sequence.
CK252271
CK252271.1 GI:39806102
EST.
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 899)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Contact: EST735909
Other ESTs: EST735909
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..899
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POC8787"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."
FEATURES
source
Query Match 32.3%; Score 499.2; DB 14; Length 899;
Best Local Similarity 90.2%; Pred. No. 9.8e-93;
Matches 534; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 ATCTTTGTTGAAAAATGGAAAAAGACGTAGGACCACTGGACCTTTGGGTGCAACAAT 60
Db 593 ATCTTTGTTGAAAAATCTAGACAAATCAGTAGGACCACTGGACCTTTGGGTGCAACAAT 534
QY 61 ATTGTTGTCCTCCAAATGTTGTTACAGGATTTTACATCCTCCGGTACTTTAGCTGAC 120
Db 533 ATGTGTGTCCTCCGAACTGGTACAGGATTTTACATCCTCCAGGTACCTTAAGTGAAC 474
QY 121 TAGGACATTCACCAATTTATTTGCGGTGCAATTAATTCGTTGGGCAATTTCCCTCCACTTG 180
Db 473 CAGGACATTCACCAATTTATTTAGCGGTGCAATTAATTCGTTGGGCAATTTCCCTCCACTAG 414
QY 181 GATTAGTCGGGGCGAAAGTCATCGGTATTTAAATTCATTCACCTAAAGAAATGTCGCCAGA 240
Db 413 GATTGGTTGGGGCAAAAGTCATCGGAATTTAAATTCATTCACCTAAAGAAATGTCGCCAGA 354
QY 241 AATCTAAGTTGTTGAACCTGGTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTTTACCCC 300
Db 393 AATCTAAGTTGTTGAACCTGGTCCGAGGCGTATTTCAGCCAGGCGTGTGTTGGTGGTTGCC 294
QY 301 ACCCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGACGAACTTACAGCAC 360
Db 293 ACCCGGTGCACTGCAGGACACCAACCAATCACCAGTCATGACGAACTTACAGCAC 234
QY 361 CATCGAAGTTACATCCAGTAGACACCCCATATACGTGGCCATCGTAGTGGCCCTAGGCGCAT 420

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||||| 233 CATCAAGATTGCAATTAGTAGACGCCCATATAGTGCATCTTAGTGGCCCTCGGCGCAT 174
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||||| 421 CAATGACCCACGCTTTGGCCCTCGATCGAGACGTGCGCCACCGCTATTCGGGGTGGATGCTG 480
|||||
||||| 173 TGATACCCATGCTCTGGCCCTCGATCGAGAGCTGGCCACCGCTATTCGGGGTGGATGCG 114
|||||
||||| 481 CCAGACGGTGTATGACAGCTTTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
|||||
||||| 113 CCACACGGTGTATGACAGCTTTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 54
|||||
||||| 541 CAAAAGCAAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGT 592
|||||
||||| 53 CAAAAGCAAGGAGGAGAAACAAAAGAGATCTCAAGTAGGCCATGTTTGT 2
|||||
RESULT 7
BI176339/c
LOCUS
DEFINITION
EST51129 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PPCAC11 5' sequence similar to
osmotin-like protein (Capsicum annuum), mRNA sequence.
BI176339
ACCESSION
VERSION
BI176339.1 GI:14642150
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 739)
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A.,
Bougrin, O., Buell, C.R., Renning, C.W., Fry, W.E. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13P-R.
Location/Qualifiers
1..739
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCAC11"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
compatible reaction"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University, Fry lab; sequencing:
The Institute for Genomic Research; whole plants were
challenged with 20,000 sporangia/ml of the compatible P.
infestans isolate US 940480. Leaf tissue was collected at
3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
in liquid nitrogen immediately upon removal. Kennebec
plants showed first symptoms of infection at 48 hours
after inoculation. NOTE: We cannot exclude the
possibility that this sequence is actually derived from
Phytophthora rather than potato."
ORIGIN
Query Match 32.1%; Score 495.8; DB 12; Length 739;
Best Local Similarity 90.3%; Pred. No. 5.1e-92;
Matches 530; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGACGTAGGACCAATGACCTTTGGTGCACAAT 60
Db 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGACGTAGGACCAATGACCTTTGGTGCACAAT 528
QY 61 ATTGTTGCTCCTCAAAATGTTGACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 120
Db 1 ATTGTTGCTCCTCAAAATGTTGACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 468
QY 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 180
Db 1 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 408
QY 181 GATTAGTCGGGGCGAAGTCTATCGGTATATTAAATCCATCAATTAAGAAATGTCACGAGA 240
Db 1 GATTAGTCGGGGCGAAGTCTATCGGTATATTAAATCCATCAATTAAGAAATGTCACGAGA 348
QY 241 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGGCGTTTACCCC 300
Db 1 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGGCGTTTACCCC 288
QY 301 ACCCGGTGCACTGACGAGGACACCAACCAATCAACGATCATGACGAAACCTTACACGAC 360
Db 1 ACCCGGTGCACTGACGAGGACACCAACCAATCAACGATCATGACGAAACCTTACACGAC 228
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATGTTAGTGGCGGTAGCGCAT 420
Db 1 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATGTTAGTGGCGGTAGCGCAT 168
QY 421 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 480
Db 1 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 108
QY 481 CCCAGACGGTGTATGGAAGTGTGCTGCTGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 540
Db 1 CCCAGACGGTGTATGGAAGTGTGCTGCTGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 48
QY 541 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 587
Db 1 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATG 1

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RESULT 8
AM039873/c 649 bp mRNA linear EST 18-MAY-2001
LOCUS EST282346 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
DEFINITION clone cLET13J13, mRNA sequence.
ACCESSION AM039873
VERSION AM039873.1 GI:5898627
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ascarids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 649)
D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,
Rönnig, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,
Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and
Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..649
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"

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FEATURES
source

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/clone="cLET13J13"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF,"
/clone_lib="tomato mixed elicitor, BTI"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
NotI; cLET - Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisocotinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

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ORIGIN

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Query Match 31.7%; Score 490.2; DB 9; Length 649;
Best Local Similarity 89.3%; Pred. No. 7.4e-91;
Matches 528; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGACGTAGGACCAATGACCTTTGGTGCACAAT 60
Db 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGACGTAGGACCAATGACCTTTGGTGCACAAT 532
QY 61 ATTGTTGCTCCTCAAAATGTTGACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 120
Db 1 ATTGTTGCTCCTCAAAATGTTGACAGGATTTGATCATCTCCGGGTACTTTAAGCTGAC 472
QY 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 180
Db 1 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 412
QY 471 CAGGACATTCACCAATTTATTTAGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 412
Db 1 CAGGACATTCACCAATTTATTTAGCGGTGCAATGAAATGCGGTGCAATTTCCCTCCACTTG 240
QY 181 GATTAGTCGGGGCGAAGTCTATCGGTATATTAAATCCATCAATTAAGAAATGTCACGAGA 240
Db 1 GATTAGTCGGGGCGAAGTCTATCGGTATATTAAATCCATCAATTAAGAAATGTCACGAGA 352
QY 241 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTACTTACCCC 300
Db 1 AATCTAAGTTGTTGAACCTGCTCCGAGGCGTACTCGGCTAGGCTGTTTGGCGGTACTTACCCC 292
QY 301 ACCCGGTGCACTGACGAGGACACCAACCAATCAACGATCATGACGAAACCTTACACGAC 360
Db 1 ACCCGGTGCACTGACGAGGACACCAACCAATCAACGATCATGACGAAACCTTACACGAC 232
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATGTTAGTGGCGGTAGCGCAT 420
Db 1 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATGTTAGTGGCGGTAGCGCAT 172
QY 421 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 480
Db 1 CAATGACCCAGCTTTGGCTCGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 112
QY 481 CCCAGACGGTGTATGGAAGTGTGCTGCTGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 540
Db 1 CCCAGACGGTGTATGGAAGTGTGCTGCTGATCGAGACGTGCGGCCACCGCTATCGGGTCCGATCGTG 52
QY 541 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGTTT 591
Db 1 CAAAGACGAAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGTTT 1

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RESULT 9

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BI432833/c 583 bp mRNA linear EST 30-APR-2003
LOCUS EST535594 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAW35 5' sequence, mRNA sequence.
ACCESSION BI432833
VERSION BI432833.1 GI:15257523
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 583)
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A.,

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TITLE	Bouiri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@igr.org This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/ Seq primer: M13F-R.

FEATURES	source	Location/Qualifiers
1.	.583	/organism="Solanum tuberosum"
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		/cultivar="Kennebec"
		/db_xref="taxon:4113"
		/clone="PPCAW35"
		/tissue_type="leaf"
		/dev_stage="6 week old"
		/lab_host="SOLR"
		/clone_lib="P. infestans-challenged potato leaf, compatible reaction"
		/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 94C480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed first symptoms of infection at 48 hours after inoculation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
ORIGIN		
Query Match	31.5%;	Score 487.2; DB 12; Length 583;
Best Local Similarity	90.0%;	Pred. No. 3.1e-90;
Matches 522; Conservative	0;	Mismatches 58; Indels 0; Gaps 0;
QY	19	TGGAAGAAAGCGTAGGACACATGCGACTTGGGTGCAACAATATTGTTGCTCTCCAAATG 78
DB	581	TGCAAAATCAGTAGGACCAATGACCTTGGGTGCAACAATATTGTTGCTCTCCGAAG 522
QY	79	TGTTACAAGGATTTGATATCTCTCGGGTACTTTAAAGCTGACTAGGACATTCACCATTTA 138
DB	521	TGGTACAAGGATTTGATATCTCTCAGGTACCTTAAGTGAACAGGACATTCACCATTTA 462
QY	139	TATTTGCGGTGCATTTGAATTCGGTGGCAATTTCCCTCCTCTGGATTTAGTCGGGGCGAAG 198
DB	461	TATTAGCCGTGCAATGAATTCGGTGCAATTTCCCTCCTCCTAGGATTTGGTGGGGCGAAG 402
QY	199	TCATCGGTATATTAAATCCATCACTAAGAATATGCCAGAAATCTAAGTTGTTGAACT 258
DB	401	TCATCGGAATATTAAATCCATCGACTAAGAATATGCCAGAAATCTAGTTGCTGAAT 342
QY	259	GGTCGAGCGGTATCGGTAGGGTGTTCGGGGTTTACCCACCGCGTGCACGAGCA 318
DB	341	GGTCAAGGCGGTATCGGGTAGGGTGTTCGGTGGTTTGGCCCAACCGGTACATTGCAAGA 282
QY	319	CACCAACCAATCACCGTCAATGCACGAACCTTACCAGCACCATCGAAGTTACATCCAG 378
DB	281	CCCAACCAATCACCGATTGGCATGAACCTCTGCCAGCAACCATCAAGATTACAAATTAG 222
QY	379	TACGACCCCATATACGTGCCATCGTAGTGCCTCTAGGCGGCATCAATGACCCACGTTTGGC 438
DB	221	TACGACCCCATATACGTGGCATTTAGTACCCCTCGGCGCATTTGATGCCCATGCTCTGGC 162
QY	439	CTCGATTCGAGACGTCGGGCGACCGGCTATTCGGGTTCGATGCTGCCAGACGGTGTATGAC 498
DB	161	CTCGATTCGAGACGTCGACCGCATTCGGGTTCGATGCTGCCACGATGATGAC 102

Qy	499	AGTTGTTGGCTACTCGATAGTGCACGACATAAGTGAAAGTCACAAAAGCAAGAAGGGAGA	558
Dd	101	AGTTGTTGGCTACTCGATAGTGCACGACATAAGTGTAGTCACAAAAGCAAGAAGGAAGA	42
Qy	559	AAACAAAGAAGATCTCAAAGTAGCCCATGTTTGTGTAAT	598
Dd	41	AAACAAAGAAGATCTCAAAGTAGCCCATGTTTTTTAACT	2

622 bp mRNA linear EST 07-MAR-2003

BF053678
EST438908 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB36B20 5' sequence, mRNA sequence.

ACCESSION BF053678
VERSION BF053678.1 GI:10807574
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 622)

van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J.,
Unterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R.,
Rønning,C.M., Fry,W.E., Tankalev,S.D. and Baker,B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>.

RESULT 10	BF053678/c
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

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ncftp://genome.arizona.edu/orcids/.
Location/Qualifiers
1. 622
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="STR36B20"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/clone_lib="potato leaves and petioles"
/notes="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN

Query Match          31.4%; Score 486; DB 10; Length 622;
Best Local Similarity 89.0%; Pred. No. 5.5e-90;
Matches 525; Conservative 0; Mismatches 65; Indels 0; Gaps 0

Qy      1  ATCTTTGTTTGA AAAAATTCGAA AAGAACCTGAGGACCACATGGGACCTTGGGTGCAACAAT 60
      |||
Db      599 ATCTTTGTTTGA AAAATCTCGACCAAGTCAGTAGGACCACATGGGACCTTGGGTGCAACAAT 540
      |||

Qy      61  ATGTGTGTCTCTCAAAATGTTGGTCAAGGATGTTACATCTCCGGGTACTTTTAAGCTGAC 120
      |||
Db      539 ATGTGTGTCTCTCGAAGCGTGGTCAAGGATGTTTACATCTCCGGGTACTTTTAAGTTGAC 480
      |||

Qy      121 TAGGACATTCACCAATTTATATTTGGCGGTGATGAAATTGGGTGGCAATTTCCCTCCACTTG 180
      |||
Db      479 CAGGGCAATTCACCAATTTATATTTGGCGGTGATGAAATTGAGTGGCATTTTCTCCACTTAG 420
      |||

Qy      181 GATTAGTTCGGGGGGGAAAGTCATCGGTATATTTAAATCCATCAACTAAAGAAATGTCCCAGA 240
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Db      419 GATTGGTCGGGGCAAAAGTCATTGGTATATTTAAATCGTCAACTAAAGAAATGTCCCAGA 360

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Qy	241	AATCTAAGTTGTTTGAAC	TGGTCCAGGCGTACTCGGCTAGGGTGT	TTGGGGTTTACCCC	300
Db	359	AATCTAGGTTGTTTAAAC	TGATTCAGGCGATATTCGGCCAGGGTGT	TTGGGGTTTACCCC	300
Qy	301	ACCGGTGCACTGCAGAC	CAACCCACCAATACACCAAGTCATGC	ACGAACCTTACCAAGCAC	360
Db	299	ACCGGTGCACTGCAGAC	CTCCAAATCACCAGTCTGACAAAGACCT	CTACCAAGCAC	240
Qy	361	CATCGAAGTTTACATCC	AGTAGTCAGACCCCATATACGTGCCATCG	TAGTGCCTCAGCGCAT	420
Db	239	CATCAAAAGTTGCAATT	AGTAGTACGACCCCATATACGTGCCATCT	TAGTGCCTCAGCGCAT	180
Qy	421	CAATGACCCACGTTTGG	CCTCGATCGAGACGTGCGGCCACCGCCT	TATCGGGTGCATGCTG	480
Db	179	TGATGACCCCAAGTTT	GTGACCTCGATCGAGACGTGCGGCCACCGCCT	TATCGGGTGCATGCTG	120
Qy	481	CCCAGACGGTGTATGGA	CAGTTGTTGGGTACTCTCGATAGTGGCAGC	ATTAAGTGAAAGTCA	540
Db	119	CCCAGACGGTGTATGGA	CAGTTGTTGGGACCTCAAAGAGGTAGCAT	TAAGTATAAGTCA	60
Qy	541	CAAAAGCAAGAGGAGGA	AAAAACAAGAGATCTCAAGTAGTCCCATGTTT	590	
Db	59	CAAAAGAAAGGAGGAAG	AAAAACAAAAGAAATCTCAATAGCCCATGTT	10	
RESULT 11					
BG130690/c					
LOCUS					
DEFINITION					
EST463582 tomato crown gall Lycopersicon esculentum cDNA clone					
cTOE1A9 5', sequence similar to putative pathogenesis-related					
protein PR P23, mRNA sequence.					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Lycopersicon esculentum (tomato)					
Lycopersicon esculentum					
Eukaryota; Viridiplantae;					
Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.					
1 (bases 1 to 539)					
van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C.,					
Rönnig,C. and Tanksley,S.					
Generation of ESTs from tomato crown gall tissue					
Unpublished (2001)					
Contact: CUGI					
Clemson University Genomics Institute					
Clemson University					
100 Jordan Hall, Clemson, SC 29634, USA					
Email: http://www.genome.clemson.edu/orders/index.html .					
FEATURES					
source					
1..639					
/organism="Lycopersicon esculentum"					
/mol_type="mRNA"					
/cultivar="TA96"					
/db_xref="taxon:4081"					
/clone="cTOE1A9"					
/tissue_type="crown gall"					
/dev_stage="crown galls from full-grown plants (8 wks					
old)"					
/lab_host="SOLR"					
/clone_lib="tomato crown gall"					
/notes="Vector: pBluescript SK(-); Site1: EcoRI; Site2:					
XbaI; Four wk old greenhouse plants were stab inoculated					
on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr,					
Cornell U.). Galls were allowed to develop for another 4					
wks, when gall tissue was frozen in liquid nitrogen."					
ORIGIN					
Query Match					
Best Local Similarity					
Matches 523; Conservative					
0; Mismatches 63; Indels					
0; Gaps					
0;					

Qy	1	ATCTTTGTTGAAAAATTTGGAAAGNACG	TAGAGCCACATGAGACCTTGGTGCACAAAT	60
Db	587	ATCTTTGTTTGGAAAAATCTCGACAAAT	TCAGTAGGGCCACATGACCTTGTGTGCAACAAT	528
Qy	61	ATTGTTGTCTCTCAAAATGCGTACAAGG	ATTGTTACATCTCCGGGTACTTTTAAGCTGAC	120
Db	527	ATTGTTGTCTCTCGAACGTGTTACAGGAT	TGTTACATCTCTCGGGTACCTTAAGTGAAC	468
Qy	121	TAGACATTCACCATTTATATTTGCGGTG	CAATTGGAATTTGCGTGGCATTTCCCTCCACTTG	180
Db	467	CAGGACATTCACCATTTATATTAGCCGT	ACAATGAATTTGATGGCATTTCCCTCCACTAG	408
Qy	181	GATTAGTCGGGGGGAAGTCAATCGGTAT	ATTTAAATCCATCAAATAAGAAATGTCGCCAGA	240
Db	407	GATTGTCGGGGGGAAGTCAATCGGTAT	ATTTAAATCCATCAAATAAGAAATGTCGCCAGA	348
Qy	241	AATCTAAGTTGTTGAACTGGTCCGAGCG	CTACCTCGGTAGGTTGTCGGGTTTACCCC	300
Db	347	AATCTAGTTGTTGAACTGGTCCGAGCG	CTACCTCGGTAGGTTGTCGGGTTTACCCC	288
Qy	301	ACCGGTGCACTCGAGGACACACCAATCA	CCAGTCTATGCGAGACCTCTACCAAGCAC	360
Db	287	ACCGGTGCACTCGAGGACACACCAATCA	CCAGTCTATGCGAGACCTCTACCAAGCAC	228
Qy	361	CATCGAAGTTACATCCAGTACGACCCCA	TATATGCTGCTAGTGCCTTAGCGGCGCAT	420
Db	227	CATCAAGTTGCAATCTGTTACGACCCCA	TATATGCTGCTAGTGCCTTAGCGGCGCAT	168
Qy	421	CAATGACCAAGTTTGGCTCTCGATCGAG	AGTCTGCGGCGCATGCTGCTGCTGCTGCTG	480
Db	167	TGATGACCCATGTTTGGCTCTCGATCAAG	ACGCTGCGGCGCATGCTGCTGCTGCTGCTG	108
Qy	481	CCAGACGGTGTATGACAGCTTGTGCGT	ACCTCGATAGTGGAGCATAGTGAAGTCA	540
Db	107	CCAGACGGTGTATGACAGCTTGTGCGT	ACCTCGATAGTGGAGCATAGTGAAGTCA	48
Qy	541	CAAAAGCAAGAGGGAGAAAAAACAAGAT	CTCAAGTAGGCCAT	586
Db	47	CAAAAGCAAGAGGGAGAAAAAACAAGAT	CTCAAGTAGGCCAT	2

RESULT 12

BI922472/c

LOCUS

DEFINITION

EST542376 tomato callus Lycopersicon esculentum cDNA clone

CLUEC77J15 5' end, mRNA sequence.

ACCESSION

BI922472

VERSION

BI922472.1

KEYWORDS

GI:16219560

SOURCE

Lycopersicon esculentum (tomato)

ORGANISM

Lycopersicon esculentum

REFERENCE

1 (bases 1 to 667)

AUTHORS

Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai, J., Uterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tankley, S.D. and Giovannoni, J.

TITLE

Generation of ESTs from tomato callus tissue (2001)

JOURNAL

Unpublished (2001)

COMMENT

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq primer: T3

Location/Qualifiers

1..667

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

FEATURES

source

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/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/clone_lib="tomato callus"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLSC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST library"
```

ORIGIN

```
Query Match 31.2%; Score 483; DB 12; Length 567;
Best Local Similarity 88.2%; Pred. No. 2.3e-89;
Matches 525; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 4 TTTGTTGAAAAATGGAAAGAACGTAGGACCAACATGGACCTTGGGTGCAACAATATT 63
Db TCTGTTGAAAAATCTCGACAAATCAGTAGGGCCACATGGACCTTGTGCAACAATATT 537
Qy 64 GTTGCTTCCAAATGTGTACAAAGATTGTTATCATCTCCGGGTACTTTAAGCTGACTAG 123
Db GTTGCTTCCGAACGTGTGTACAAAGATTGTTATCATCTCCGGGTACTTAAAGTGAACCA 477
Qy 124 GACATTCACCAATTATTTGCGGTGCTATTGAATTCGTTGGGTCATTTCCCTCCACTTGGAT 183
Db GACATTCACCAATTATTTAGCCGTACAAATGAATTCGATGGATTTCCCTCCACTAGAT 417
Qy 184 TAGTCGGGGCGAAAGTCATCGGTATATTAAATPCCATCAACTAAAGAAATGTCCAGAAAT 243
Db TGGTCGGGGCGAAAGTCATTTGAATATTAAATPCCATCAACTAAAGAAATGTCCAGAAAT 357
Qy 244 CTAAGTTGTGAACGTCCGAGGCGTACTCGCTAGGGTGTGGCGGTATCCGCCACC 303
Db CTAGGTTGTAAACTGGTCCGAGGCGTACTCGGCCAGGGTGTGGTGGTGTGGCGGCCACC 297
Qy 304 CGGTGCATCGAGGACACACCAATCACCAGTCATGCAGAACTCTACCGAGCACCAT 363
Db CGGTACATTCGAAGACCCACCAATCACCAGTCGTGACATGACCTCTACCGAGCACCAT 237
Qy 364 CGAAGTTAGATCCAGTAGACCCCATATAGTGCCATCGTAGTGGCCCTTAGCGGCATCAA 423
Db CAAAGTTGCAATTCGTACGACCCCATATAGTGCCATCTTAGTGCCCTCGGTGCAATGA 177
Qy 424 TGACCCAGCTTTGGCTCGATCGACGCTCGSCCACCCTATCGGGTTCGATGCTGCC 483
Db TGACCCATGTTGGCTCGATCGACGCTCGACCCACCCTATTTGGGTTCGACCGCCGCC 117
Qy 484 AGACGGTGTATGACAGTGTGTGCGTACTCGATAGTGGCAGCATAAAGTGAAGTCACAA 543
Db AGACGGTGTATGACAGTGTGTGCGTACTCGAAAGTGGCAGCATAAAGTGAAGTCACAA 57
Qy 544 AGCAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAAAT 598
Db AAGCAAGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGGAAT 2
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```
RESULT 13
AW031249/c 585 bp mRNA linear EST 18-MAY-2001
LOCUS
DEFINITION
ES2724624 tomato callus, TAMU Lycopersicon esculentum cDNA clone
cLSC34F24 similar to osmotin-like protein TPM-1 precursor (PR P23),
mRNA sequence.
ACCESSION
AW031249
VERSION
AW031249.1 GI:5889926
KEYWORDS
EST.
SOURCE
Lycopersicon esculentum (tomato)
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
```

```
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 585)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 Prime sequence.
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FEATURES

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source
1..585
/organism="Lycopersicon esculentum"
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC34F24"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/clone_lib="tomato callus, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni laboratory; cLSC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
```

ORIGIN

```
Query Match 31.1%; Score 480.8; DB 9; Length 585;
Best Local Similarity 89.0%; Pred. No. 6.6e-89;
Matches 518; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 19 TGGAAAGAACGATGAGACCAACATGGACCTTGGGTGCAACAATATTGTTCCTCCAAATG 78
Db TCGACAAATCAGTAGGNCACATGGACCTTGTGCAACAATATTGTTCCTCCGACG 524
Qy 79 TGGTACAGGATTGTACATCTCCGGTACTTTAGCTGACTAGGACATTCACATTTA 138
Db TGGTACAGGATTGTACATCTCCGGTACTTCCTCCGGTACTTCACATTTA 464
Qy 139 TATTGCGGTGCAATGAATTTGGTGGCATTTCCCTCCACTTGGATTAGTCGGGCGGAAAG 198
Db TATTGCGGTGCAATGAATTTGGTGGCATTTCCCTCCACTTGGATTAGTCGGGCGGAAAG 404
Qy 199 TCATCGGTATATTAAATPCCATCAACTAAAGAAATGTCCAGAAATCTAAGTTGTTGAACT 258
Db TCATCGGTATATTAAATPCCATCAACTAAAGAAATGTCCAGAAATCTAAGTTGTTGAACT 344
Qy 259 GGTCCGAGGGTACTCGGCTAGGGTGTGGCGGTTTACCCACCCGGTGCACATGACGA 318
Db GGTCCGAGGGTACTCGGCGAGGGTGTGGTGGTTTGGCCCGCCCGGTACATTCGAAGA 284
Qy 319 CACACACCAATCACCAGTCATCGCAGAACCTCTACAGCACCCTACAGCACCCTCAAGTTACATCCAG 378
Db CCCCACCAATCACCAGTCTGACATGAACCTCTACAGCACCCTCAAGTTGCAATTCG 224
Qy 379 TAGCACCCCATATACGTGCCATCGTAGTGCCCTTAGCGCATCAATGACCCAGTTTGGC 438
Db TAGCACCCCATATACGTGCCATCTTAGTGCCCTTAGCGCATCAATGACCCAGTTTGGC 164
Qy 439 CTCGATCGAGACGTCCGGCCACCCCTTATCGGGTTCGATGTGCCCGCCAGCGGTGTATGGAC 498
Db CTCGATCGAGACGTCCGACCCCTTATTTGGGGTTCGACCGCCCGCCAGCGGTGTATGGAC 104
Qy 499 AGTTGTTGGTACTCTCGATAGTGGCAGCATAAGTGAAGTCAAAAGCAAGAGGAGA 558
Db AGTTGTTGGTACTCTCGAAAGTGGCAGCATAAGTGAAGTCAAAAGCAAGAGGAGA 44
```


/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory;_cIEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

ORIGIN		Query Match	30.7%;	Score 474.4;	DB 9;	Length 583;
		Best Local Similarity	88.6%;	Pred. No. 1.4e-87;		
		Matches 514;	Conservative 0;	Mismatches 66;	Indels 0;	Gaps 0;
QY	19	TCGAAAGAACGATAGGACACATGACCTTGGTGCAACAATATTGTTGTCTCTCAATG	78			
Db	581	TCGACAAATCAGTAGGGCCACATGACCTTGTGCAACAATATTGTTGTCTTCGAACG	522			
QY	79	TGGTACAGGATTGTATCATCTCCGGGTACTTTAAGCTGACTAGGACATTCACCATTTA	138			
Db	521	TGGTACAGGATTGTATCATCTTCGGGTACCGTAAGTGAACCCAGGACATTCACCATTTA	462			
QY	139	TATTTGCGGTGCATTGAATTGCGTGGCATTTCCCTCCCACTTCGATTAGTCGGGGCGAAAG	198			
Db	461	TATTAGCGGTACAATGAATTGCATGGCATTTCCCTCCCACTAGGATTGTCGGGGCGAAAG	402			
QY	199	TCATCGGTATTATAATCCATCACTAAAGAAATGCCAGAAATCTAAGTTGTGAAT	258			
Db	401	CAATTGGAATATTAAATCCATCGACTAAAGAAATGCCAGAAATCTAAGTTGTGAAT	342			
QY	259	GGTCCGAGCGTACTCGGTAGGGTGTGGGGTTTACCCACCCGGTGCACTGCAGGA	318			
Db	341	GGTCCAGGCGTACTCGGCCAGGGTGTGGGGTTTCCGCCACCCGGTACATTGCAGA	282			
QY	319	CACCAACCAATCACCACTGTCATGCAAGAACCTCTACCAAGCAATCGAAGTTACATCCAG	378			
Db	281	CCCCACCAATCACCACTGTCATGAACCTCTACCAAGCAATCGAAGTTGCAATTCG	222			
QY	379	TACGACCCCATATAGTCCATCGTAGTGGCCCTAGCGGCATCAATGACCCACGTTTGGC	438			
Db	221	TACGACCCCATATAGTCCATCTTAGTGGCCCTCGGTGCATTGATGACCCATGTTTGGC	162			
QY	439	CTCGATCGAGAGCTCGGGCCACCGCCTATCGGGGTGATGCTGCCCGACGCGGTATGGAC	498			
Db	161	CTCGATCAAGAGCTCGACCCCGCCTATTGGGGTGCACGCCCGCAGACGCGGTATGGAC	102			
QY	499	AGTTGTTGGGTACCTCGATAGTGGCAGCATTAAGTGAAGTCAAAAGCAAGAGAGGAGA	558			
Db	101	AGTTGTTGGGTACCTCGAAGTGGCAGCATTAAGTGAAGTCAAAAGCAAGAGAGGAGA	42			
QY	559	AAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAAT	598			
Db	41	AAACAAAGAGATCTCAAGTAGGCCATGTTGTTGAAAT	2			

Search completed: August 18, 2004, 16:04:26
Job time : 3636.85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:32:09 ; Search time 552.632 Seconds
(without alignments)
11884.422 Million cell updates/sec

Title: US-10-051-307-3
Perfect score: 1546
Sequence: 1 atctctgttgaaaaaattg.....tggtgaagtgtgtgttc 1546

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1532.2	99.1	1546	6	Abk90562 Potato pr
2	1362.4	88.1	1595	6	Abk90560 Potato pr
3	1334.4	86.3	1598	6	Abk90561 Potato pr
4	500	32.3	3033	2	Aav52754 Nicotiana
5	500	32.3	3033	2	Aax16340 Tobacco o
6	450.4	29.1	883	2	Aaq15269 Osmotin-1
7	450.4	29.1	884	2	Aaq15270 Encodes C
8	448.4	29.0	741	2	Aav68641 Nucleotid
9	382.2	24.7	1004	2	Aaq21414 Encodes o
10	288.2	13.5	906	3	Aac47993 Arabidops
11	207.8	13.4	902	3	Aac47227 Arabidops
12	207.2	13.4	735	6	Abz14313 Arabidops
13	207.2	13.4	735	7	Abz42096 Arabidops
14	207.2	13.4	735	7	Ada68525 Arabidops
15	207.2	13.4	950	6	Abn98566 Arabidops
16	180.6	11.7	875	5	Aac84839 Sunflower
17	172.4	11.2	771	3	Aaz22511 Asparagus
18	159.2	10.3	900	1	Aan90842 Fragment
19	159.2	10.3	900	2	Aav62808 Tobacco P
20	159.2	10.3	900	2	Aav72992 PR-R majo
21	153.8	9.9	549	5	Aac5150 Arabidops
22	152.6	9.9	910	4	Aad04241 Sunflower
23	143.8	9.3	2000	7	Ada71704 Rice gene

C 24	132.4	8.6	500	3	AAA40422	Aaa40422 Potato in
C 25	128.4	8.3	693	2	AAQ58991	Aaq58991 Diospyros
C 26	127.4	8.2	627	2	AAQ58992	Aaq58992 Diospyros
C 27	124.8	8.1	894	2	AAQ91491	Aaq91491 Zeamatin
C 28	116.2	7.5	705	1	AAAN40215	Aan40215 Gene enco
C 29	115.4	7.5	343	6	ABQ85936	Abq85936 Arabidops
C 30	112	7.2	1932	7	ADA71064	Ada71064 Rice gene
C 31	109.4	7.1	950	2	AAQ06184	Aaq06184 PR-R majo
C 32	109.4	7.1	1970	7	ADA71063	Ada71063 Rice gene
C 33	104.4	6.8	808	2	AAV28688	Aav28688 Ripening
C 34	102.4	6.6	669	7	ADA59630	Ada59630 Rice gene
C 35	101	6.5	1309	2	AAQ4913	Aaq4913 PING152CV
C 36	101	6.5	1309	2	AAQ4914	Aaq4914 PING323CV
C 37	95.6	6.2	621	1	AAAN70934	Aan70934 DNA seque
C 38	94.4	6.1	621	6	ABQ78707	Abq78707 Nucleotid
C 39	94.4	6.1	621	9	AAQ59196	Aaq59196 Modified
C 40	94	6.1	621	1	AAAN70933	Aan70933 DNA seque
C 41	94	6.1	621	6	ABQ78703	Abq78703 Nucleotid
C 42	94	6.1	621	9	AAQ59192	Aaq59192 Thaumatin
C 43	94	6.1	639	1	AAAN50328	Aan50328 Sequence
C 44	82	5.3	961	1	AAAN20003	Aan20003 Preprotha
C 45	81.4	5.3	624	2	AAAT06312	Aat06312 Thaumatin

ALIGNMENTS

RESULT 1
ABK90562
ID ABK90562 standard; DNA; 1546 BP.
XX
AC ABK90562;
XX
DT 15-NOV-2002 (first entry)
XX
DE Potato proteinase inhibitor 1 (pinl) gene promoter isoform III.
XX
KW Potato; proteinase inhibitor 1; pinl; promoter; ds; plant;
KW Controlled Environmental Agriculture; crop cultivation.
XX
OS Solanum tuberosum.
XX
XX WO200259333-A2.
XX
PD 01-AUG-2002.
XX
PF 18-JAN-2002; 2002WO-US001287.
XX
PR 23-JAN-2001; 2001US-0263224P.
XX
XX (DAIZ/) DAI Z.
XX (SHIL/) SHI L.
XX (HOOK/) HOOKER B S.
XX
XX Dai Z, Shi L, Hooker BS;
XX WPI; 2002-608457/65.
XX
XX New proteinase inhibitor 1 (pinl) or aminotransferase (amt) gene promoter
XX Isoforms derived from potato, useful in manipulating expression of genes
XX and in Controlled Environmental Agriculture for heterologous protein
XX production.
XX
XX Claim 2; Fig 3; 43pp; English.
XX
XX The invention relates to polynucleotides having proteinase inhibitor 1
XX (pinl) or aminotransferase (amt) gene promoter activity. Isoforms of pinl
XX and amt gene promoters are useful in manipulating expression of genes,
XX particularly in transformed plant cells. The gene promoters are useful in
XX constructing gene expression vectors and in Controlled Environmental
XX Agriculture for heterologous protein production. The vectors are useful
XX in facilitating the expression and/or secretion of heterologous proteins
XX in cell culture or by crop cultivation. The new gene promoter isoforms

CC provide high level, stable and controllable expression that is
 CC temporarily, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform

XX
 SQ Sequence 1546 BP; 501 A; 270 C; 284 G; 490 T; 0 U; 1 Other;

Query Match	99.1%;	Score 1532.2;	DB 6;	Length 1546;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1538;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	ATCTTTGTTTCAAAAATGGAAGAAGCGTAGGACACATGACCTTGGGTGCAACAAT	60	
DB	1	ATCTTTGTTTCAAAAATGGAAGAAGCGTAGGACACATGACCTTGGGTGCAACAAT	60	
QY	61	ATTCTTGTCTCCAAATGTGTGTCACAGGATGTTTACATCTCCGGGACCTTTAAGCTGAC	120	
DB	61	ATTCTTGTCTCCAAATGTGTGTCACAGGATGTTTACATCTCCGGGACCTTTAAGCTGAC	120	
QY	121	TAGGACATTCACCAATTTATATTTGCGGTGCATTCGAATTCGTCGCAATTCCTCCCACTTG	180	
DB	121	TAGGACATTCACCAATTTATATTTGCGGTGCATTCGAATTCGTCGCAATTCCTCCCACTTG	180	
QY	181	GATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCCAGA	240	
DB	181	GATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAAGAAATGTCCAGA	240	
QY	241	AATCTAAGTTTGAATCTGTCAGGCGTACTCGGCTAGGGTGTGTCGGGTGTTTACCCC	300	
DB	241	AATCTAAGTTTGAATCTGTCAGGCGTACTCGGCTAGGGTGTGTCGGGTGTTTACCCC	300	
QY	301	ACCGGTGCTACTGAGGACACCAACATCACCAGTCATGCACGAACTCTTACCAGCAC	360	
DB	301	ACCGGTGCTACTGAGGACACCAACATCACCAGTCATGCACGAACTCTTACCAGCAC	360	
QY	361	CATCGAAGTTACATCGAGTACGACCCCATATACGTGCCATCTGATGTCCTTACGGCGCAT	420	
DB	361	CATCGAAGTTACATCGAGTACGACCCCATATACGTGCCATCTGATGTCCTTACGGCGCAT	420	
QY	421	CAATGACCCAGCTTGGCTCGATCGAGAGCTCGGCCACCGCTATCGGGGTGATGCTG	480	
DB	421	CAATGACCCAGCTTGGCTCGATCGAGAGCTCGGCCACCGCTATCGGGGTGATGCTG	480	
QY	481	CCCAGACGCTGTATGACAGTGTGTCGTACTCGATAGTGGCAGCATAAAGTGAAGTCA	540	
DB	481	CCCAGACGCTGTATGACAGTGTGTCGTACTCGATAGTGGCAGCATAAAGTGAAGTCA	540	
QY	541	CAAAAGCAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	600	
DB	541	CAAAAGCAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT	600	
QY	601	ATATGTGGACAAATATTTTGTGCTATATATAGGGATATGGCGCTTTTGGCACTA	660	
DB	601	ATATGTGGACAAATATTTTGTGCTATATATAGGGATATGGCGCTTTTGGCACTA	660	
QY	661	TGGATATTAATCGTATTATATAACAATATCATCTTTGACTAATTAATAACAATAATAT	720	
DB	661	TGGATATTAATCGTATTATATAACAATATCATCTTTGACTAATTAATAACAATAATAT	720	
QY	721	TACAATATGATTTGTTAAACCTGAGGTGGCAAAATGTAAGAGCGCCCTAATAATTA	780	
DB	721	TACAATATGATTTGTTAAACCTGAGGTGGCAAAATGTAAGAGCGCCCTAATAATTA	780	
QY	781	TTATTTATGAATATAGACTATAGTACAAAGTGAACCTTTATTTGGTGATTAACCTGGACAT	840	
DB	781	TTATTTATGAATATAGACTATAGTACAAAGTGAACCTTTATTTGGTGATTAACCTGGACAT	840	
QY	841	ATAAATCTGTATCGTACGAGCTTTCTTAAACCTAATATTAATAAAGCAGCTATTTT	900	
DB	841	ATAAATCTGTATCGTACGAGCTTTCTTAAACCTAATATTAATAAAGCAGCTATTTT	900	
QY	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTTATGTCCTATTTTACTTTTATCG	960	
DB	901	AATATTTTTCGTGGCCAAAGTTTCTTGCATATCTTATGTCCTATTTTACTTTTATCG	960	

QY	961	TTCTAGCCTTTCTAGTAGCCTTTGACATATAAAAAATCAAAAAATTTGAAAGTAAAAAT	1020	
DB	961	TTCTAGCCTTTCTAGTAGCCTTTGACATATAAAAAATCAAAAAATTTGAAAGTAAAAAT	1020	
QY	1021	AGTTTTTTTTTCATATTTACTCGTATGGATCAATTTGTTAGATCAATGTGAATATACAAATC	1080	
DB	1021	AGTTTTTTTTTCATATTTACTCGTATGGATCAATTTGTTAGATCAATGTGAATATACAAATC	1080	
QY	1081	ATTCTGATTTTAAAAATCATAACTATTCTGATGATGGAACGCTATGTTGATTCGTGAC	1140	
DB	1081	ATTCTGATTTTAAAAATCATAACTATTCTGATGATGGAACGCTATGTTGATTCGTGAC	1140	
QY	1141	AGTCTTTGATTTTCTTAAGTCTGGATTCGAGTCACAACTTTTGTAGTGCRAATATCTATT	1200	
DB	1141	AGTCTTTGATTTTCTTAAGTCTGGATTCGAGTCACAACTTTTGTAGTGCRAATATCTATT	1200	
QY	1201	AAAAGAACCCCTATTGATGCAAAAAGTCAATAAATATTTAATATCATNCITTTATTTT	1260	
DB	1201	AAAAGAACCCCTATTGATGCAAAAAGTCAATAAATATTTAATATCATNCITTTATTTT	1260	
QY	1261	TTACGATCGAGCATGGATACATTTACTAATTAATAAATAAATTGGAAGAAATTGATCGACA	1320	
DB	1261	TTACGATCGAGCATGGATACATTTACTAATTAATAAATAAATTGGAAGAAATTGATCGACA	1320	
QY	1321	AGTCATCAAGCTTATCGTCGATCCACATTCCTTAAACGTTAGTATGGCTGCTTTTAGAGA	1380	
DB	1321	AGTCATCAAGCTTATCGTCGATCCACATTTAAATTAACGTTAGTATGGCTGCTTTTAGAGA	1380	
QY	1381	AAACAGTGGATCATATAAATTAGTTTCCCTATCTCTTATATAAATCTATATATATACC	1440	
DB	1381	AAACAGTGGATCATATAAATTAGTTTAAATAATCTCTTATATAAATCTATATATATACC	1440	
QY	1441	TCTAATACTAATGATCATCTACACACAAATATAAATCTTAGATCTTTTAAAGAAATGCA	1500	
DB	1441	TCTAATACTAATGATCATCTACACACAAATATAAATCTTAGATCTTTTAAAGAAATGCA	1500	
QY	1501	GAATTAATGAGGCAATAAAGTCTATGTTGAAAGTGGTGGCTTTTC	1546	
DB	1501	GAATTAATGAGGCAATAAAGTCTATGTTGAAAGTGGTGGCTTTTC	1546	

RESULT 2
 ABK90560
 ID ABK90560 standard; DNA; 1595 BP.
 XX
 AC ABK90560;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform I.
 XX
 KW Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;
 KW Controlled Environmental Agriculture; crop cultivation.
 XX
 OS Solanum tuberosum.
 XX
 PN WO200259333-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-JAN-2002; 2002WO-US001287.
 XX
 PR 23-JAN-2001; 2001US-0263224P.
 XX
 PA (DAIZ/) DAI Z.
 PA (SHIL/) SHI L.
 PA (HOOK/) HOOKER B S.
 XX
 PI Dai Z, Shi L, Hooker BS;
 XX
 DR WPI; 2002-608457/65.
 XX

PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
PT isoforms derived from potato, useful in manipulating expression of genes
PT and in Controlled Environmental Agriculture for heterologous protein
PT production.

XX Claim 2; Fig 1; 43pp; English.

CC The invention relates to polynucleotides having proteinase inhibitor 1
CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
CC and amt gene promoters are useful in manipulating expression of genes,
CC particularly in transformed plant cells. The gene promoters are useful in
CC constructing gene expression vectors and in Controlled Environmental
CC Agriculture for heterologous protein production. The vectors are useful
CC in facilitating the expression and/or secretion of heterologous proteins
CC in cell culture or by crop cultivation. The new gene promoter isoforms
CC provide high level, stable and controllable expression that is
CC temporally, environmentally, or developmentally regulatable. This
CC sequence represents a potato pin1 gene promoter isoform

SQ Sequence 1595 BP; 510 A; 291 C; 297 G; 497 T; 0 U; 0 Other;

Query Match 88.1%; Score 1362.4; DB 6; Length 1595;
Best Local Similarity 94.1%; Pred. No. 1.2e-297;
Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

QY	1	ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT	60
DB	49	ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT	108
QY	61	ATTGTGTCCTCCAAATGTTGTACAGGATGTTTACATCTCCGGGTACTTTAAGCTGAC	120
DB	109	ATTGTGTCCTCCAAATGTTGTACAGGATGTTTACATCTCCGGGTACTTTAAGTGTAC	168
QY	121	TAGGACATTCACATTTATATTTCCGGTGCATGAAATGGGTGGCATTTCCCTCCACTTG	180
DB	169	CAGGCAATTCACATTTATATTTCCGGTGCATGAAATGGGTGGCATTTCCCTCCACTTG	228
QY	181	GATTAGTCGGGGCAAGTATCGTATATTAATCCATCAACTAAGAAATGTCGCCAGA	240
DB	229	GATTAGTCGGGGCAAGTATCGTATATTAATCCATCAACTAAGAAATGTCGCCAGA	288
QY	241	AATCTAAGTTGTTGAACTGGTCCGAGGCGTACTCGGTGAGGTGTTTGGGGGTTTACCCC	300
DB	289	AATCTAAGTTGTTGAACTGGTCCGAGGCGTACTCGGTGAGGTGTTTGGTGGTTTGGCCC	348
QY	301	ACCGGTGCACTGAGGACACCAACAATCACAGTATGACAGCAACCTCTACGACAC	360
DB	349	ACCGGTGCACTGAGGACACCAACAATCACAGTATGACAGCAACCTCTACGACAC	408
QY	361	CATCGAAGTTACATCCAGTACGCCATATACGTGCGCATCGTAGTCCCTTAGCGGCAT	420
DB	409	CATCGAAGTTACATCCAGTACGCCATATACGTGCGCATCGTAGTCCCTTAGCGGCAT	468
QY	421	CAATGACCCACGTTGGCTCGATCGAGACGTCCGCCACCGCCCTATCGGGGTGATGCTG	480
DB	469	CAATGACCCACGTTGGCTCGATCGAGACGTCCGCCACCGCCCTATCGGGGTGATGCTG	527
QY	481	CCCAGACGCTGATGGAAGTGTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA	540
DB	528	CCCAGACGCTGATGGAAGTGTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA	587
QY	541	CAAAAGCAAGGAGGAGAAAACAAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT	600
DB	588	CAAAAGCAAGGAGGAGAAAACAAAAGATCTCAAGTAGCCCATGTTTGTGAAATTT	647
QY	601	ATATGTGACAAATATTTTGGTACTTTATATATAGGATATAGCGGCTTTTGGCACTA	660
DB	648	ATATGTGACAAATATTTTGGTACTTTATATATAGGATATAGCGGCTTTTGGCACTA	707
QY	661	TGGATATTAATCGTATATATAACAATATCATCTTTGACTAATTATAAACAATAATAT	720
DB	708	CGGATATTAATCGTATATATAACAATATCATCTTTGACTAATTATAAACAATAATAT	767

QY	721	TACAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCGGCTAATAATTA	780
DB	768	TACAATATGATTTGGTAAACGTTGAGGTGGCAAAATGTATAAGAGCGGCTAATAATTA	827
QY	781	TTATTTATGAATATAGACTATAGTTACAAGTGAACCTTTTATTTGGTGAFAACTTGGACAT	840
DB	828	TTATTTATGAATATAGCTATAGTTACAAGTGAACCTTTTATTTGGTGAFAACTTGGACAT	887
QY	841	ATAAATCTGTATCGTGACGGAACCTTTCTTAAATCTAAATATTAATAAGAGAGCTATTTT	900
DB	888	ATAAATCTGTATCGTGACGGAACCTTTCTTAAATCTAAATATTAATAAGAGAGCTATTTT	947
QY	901	ATATTTTTCGTGGCCAAAGTTCTTGTGACATCTATCTATGCCCATTCTTTTATCTG	960
DB	948	CAGATTTTTCGTGGCCAAAGTTCTTGTGACATCTATCTATGCCCATTCTTTTATCTG	1007
QY	961	TTCTAGCCCTCTAGGTACGCGTTTGAACATATAAATCATATAAATGGAAGTGAATAAT	1020
DB	1008	TTCTAGCCCTCTAGGTACGCGTTTGAACATATAAATCATATAAATGGAAGTGAATAAT	1067
QY	1021	AG---TTTTTTTTCATATTACTCGTATGATCATTTTGTGTAGATCAATGTGAATATACAA	1077
DB	1068	AGTTTTCATATTACTCGTATGATCATTTTGTGTAGATCAATGTGAATATACAA	1127
QY	1078	ATCATTTCTGATTTTAAATCATAACTATTTCTGATGATGGAACGCTATGATGCTG	1137
DB	1128	ACATTTCTGATTTTAAATCATAACTATTTCTGATGATGGAACGCTATGATGCTG	1184
QY	1138	GACAACTGTTTGAATTTTAACTGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1197
DB	1185	GACAACTGTTTGAATTTTAACTGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1244
QY	1198	ATTAAAGAACCCCTTATTTGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1255
DB	1245	ATTAAAGAACCCCTTATTTGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1304
QY	1256	TATTTTTCATGTCGGAGCATGATCAATTTACTAATAATAAATAAATGGAAGATTTGAT	1315
DB	1305	TATTTTTCATGTCGGAGCATGATCAATTTACTAATAATAAATAAATGGAAGATTTGAT	1364
QY	1316	CGACAACTCATCAAGCTTATCGTATGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1375
DB	1365	CGACAACTCATCAAGCTTATCGTATGATGCAAAAGTCAATAA---TATTTAATATCATNCTTTAT	1424
QY	1376	AGAGAAACAACTGATCATGATTAATTTAGTTTTCCTCTATCTCTATATAATCTATAT	1435
DB	1425	AGAGAAACAACTGATCATGATTAATTTAGTTTTCCTCTATCTCTATATAATCTATAT	1484
QY	1436	ATACCTCTTAAATGCAATCACTTAACACAAATATAAATCTAGATTTCTTTAAGAAA	1495
DB	1485	ATACCTCTTAAATGCAATCACTTAACACAAATATAAATCTAGATTTCTTTAAGAAA	1544
QY	1496	TTGCAAGATTAATGAGGCAAAATAGTCTATGTTGGAAGTTGGTGGCTTTC	1546
DB	1545	TTGCAAGATTAATGAGGCAAAATAGTCTATGTTGGAAGTTGGTGGCTTTC	1595

RESULT 3

ABK90561
ID ABK90561 standard; DNA; 1598 BP.

XX ABK90561;

XX 15-NOV-2002 (first entry)

DE Potato proteinase inhibitor 1 (pin1) gene promoter isoform II.

XX Potato; proteinase inhibitor 1; pin1; promoter; ds; plant;

KW Controlled Environmental Agriculture; crop cultivation.

XX Solanum tuberosum.

XX WO200259333-A2.

XX PD 01-AUG-2002.
 XX PF 18-JAN-2002; 2002WO-US001287.
 XX PR 23-JAN-2001; 2001US-0263224P.
 XX PA (DAIZ/) DAI Z.
 XX PA (SHIL/) SHI L.
 XX PA (HOOK/) HOOKER B S.
 XX PI Dai Z, Shi L, Hooker BS;
 XX DR WPI; 2002-608457/65.
 XX PT New proteinase inhibitor 1 (pin1) or aminotransferase (amt) gene promoter
 PT isoforms derived from potato, useful in manipulating expression of genes
 PT and in Controlled Environmental Agriculture for heterologous protein
 PT production.
 XX PS Claim 2; Fig 2; 43pp; English.
 CC The invention relates to polynucleotides having proteinase inhibitor 1
 CC (pin1) or aminotransferase (amt) gene promoter activity. Isoforms of pin1
 CC and amt gene promoters are useful in manipulating expression of genes,
 CC particularly in transformed plant cells. The gene promoters are useful in
 CC constructing gene expression vectors and in Controlled Environmental
 CC Agriculture for heterologous protein production. The vectors are useful
 CC in facilitating the expression and/or secretion of heterologous proteins
 CC in cell culture or by crop cultivation. The new gene promoter isoforms
 CC provide high level, stable and controllable expression that is
 CC temporarilly, environmentally, or developmentally regulatable. This
 CC sequence represents a potato pin1 gene promoter isoform.
 XX SQ Sequence 1598 BP; 507 A; 299 C; 300 G; 492 T; 0 U; 0 Other;
 Query Match 86.3%; Score 1334.4; DB 6; Length 1598;
 Best Local Similarity 93.8%; Pred. No. 2.6e-291;
 Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;
 QY 1 ATCTTTGTTTCAAAATTTGAAAGACGTTAGGACCAACATGACCTGGTGGCAACAT 60
 DB 49 ATCTTTGTTTGAATAATTTGAAAGAACGTTAGGACCAACATGACCTGGTGGCAACAT 108
 QY 61 ATTCTGTGCTCCAAATTTGTTCAAGGATTTTACATCTCCGGGTACTTTAAGCTGAC 120
 DB 109 ATTGTTGCTCCAAATTTGTTCAAGGATTTTACATCTCCGGGTACTTTAAGCTGAC 168
 QY 121 TAGGACATTTACCAATTTATTTGCGGTGCAATTTGCGGTGCAATTTCCCTCCACTTG 180
 DB 169 TAGGACATTTACCAATTTATTTGCGGTGCAATTTGCGGTGCAATTTCCCTCCACTTG 228
 QY 181 GATTAGTCCGGGCGAAAGTTCATCGGTATTTAAATCCATCACTAAAGAAATGTCACAGA 240
 DB 229 GATTAGTCCGGGCGAAAGTTCATCGGTATTTAAATCCATCACTAAAGAAATGTCACAGA 288
 QY 241 AATCTAAGTTGTTGAATCGTGGTCCGCTGCTGCGGTAGGGTGTGGGGTTTACCCC 300
 DB 289 AATCTAAGTTGTTGAACTGTTCCAAAGCGTACTCGGCTAGGGTGTGGGGTTTACCCC 348
 QY 301 ACCGGGTGCACTGAGACACCAACCAATCCAGTTCATGCAACCTCTACACAGCAC 360
 DB 349 ACCGGGTGCACTGAGACACCAACCAATCCAGTTCATGCAACCTCTACACAGCAC 408
 QY 361 CATCGAAGTTACATCCAGTACGCCCATATATCGTGCATCGTAGTCCCTTAGGGGCGAT 420
 DB 409 CAACGAAGTTACATCCAGTACGCCCATATATCGTGCATCGTAGTCCCTTAGGGGCGAT 468
 QY 421 CAATGACCCAGTTTGGCCCTGATCGAGAGCGTGGGCCACCGCTATCGGGGTGATGCTG 480
 DB 469 CAATGACCCAGTTTGGCCCTGATCGAGAGCGTGGGCCACCGCTATCGGGGTGATGCTG 527
 QY 481 CCCAGACGGTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAGTGAAGT 538

DB 528 CCCAAACGATGTATGGACAGTTGTTGGCGGTACCTTCGATAGTGCAGCATTAAGTGAAGT 587
 QY 539 CACAAAGCAAGAGGAGGAGAAACAAAGAAAGAGATCTCAAGTAGCCCATTTGTTGAAT 598
 DB 588 CACAAAGCCAGAGGAGGAGAAACCAAGAAAGAGATCTCAAGTAGCCCATTTGTTGAAT 647
 QY 599 TTATATGTGGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 658
 DB 648 TTATATGTGGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 707
 QY 659 TATGATATTAATCGTATTTATATAACAATATCATCTTTGACTAATTAATAACAATAAT 718
 DB 708 TACGGATATTAATCGTATTTATATAACAATATCATCTTTGACTAATTAATAACAATAAT 767
 QY 719 ATTCAATATGATTTGTTAAACGTTAGGTGGCAAAATGTATAAGAGCGGCTTAATATT 778
 DB 768 ATTCAATATGATTTGTTAAACGTTAGGTGGCAAAATGTATAAGAGCGGCTTAATATT 827
 QY 779 RAATATTTTATGATATATAGACTATAGTTTACAAGTCACTTTTATTTGGTGAATCTGGAC 838
 DB 828 RAATATTTTATGATATATAGACTATAGTTTACAAGTCACTTTTATTTGGTGAATCTTTGAC 887
 QY 839 ATATAAACTCTGTATCGTGACGGAACCTTTCTTAAAACTAAATATTAAAAAGCAGCTATT 898
 DB 888 ATATAAACTCTGTAACTGTGACGGAATTTTCTTAAAACTAAATATTAAAAAGCAGCTATT 947
 QY 899 TTAATATTTTGGTGGCAAAAGTTCTTGTGATCTTATCTATGCCCCATTTTACTTTTAT 958
 DB 948 TTAAGATTTTGGTGGCAAAAGTTCTTGTGATCTTATCTATGCCCCATTTTACTTTTAT 1007
 QY 959 CGTTCTAGCTTCTAGGTACGCGTTTGAACATAAAAAATCAATAAAAAATGGAAGTAAAAA 1018
 DB 1008 CGTTCTAGCTTCTAGGTACGCGTTTGAACATAAAAAATCAATAAAAAATGGAAGTAAAAA 1067
 QY 1019 TTAG---TTTTTTTTCATATTTACTCGTATGATGATTTGTTAGATCAATGTGAATATATAC 1075
 DB 1068 TTAGTTTTTTTTTTTTTTCATATTTACTCGTATGATGATTTGTTAGATCAATGTGAATATATAC 1127
 QY 1076 AAATCATTTCTGATTTTAAATCATAAATCTATTTCTGATGATGGAACGTTATGTTGATTC 1135
 DB 1128 AAACCATTTCTGATTTTAAATCACAACCATTTCTGCTAAATGCGGAGTCTAT-GTGATTC 1186
 QY 1136 GTGCAAGTGTGATTTTATTTCTAAGTCTGATTTGGAGTCAACAATTTTGTGCAATAT 1195
 DB 1187 GTGCAAGTGTGGA-TTATTTCTAGTCTAGATTTGGAGTCAACAATTTTGTGCAATAT 1245
 QY 1196 CTATTAAGAAACCCCTATTTGATGCAAAAGTCAATAAA--TATTTAATATCATNCTTTA 1253
 DB 1246 CTATTAAGAAACCCCTATTTGATGCAAAATATCTATTAAGAAACCCCTATTTCACTTTTA 1305
 QY 1254 TTTATTTTACGATCGGAGCATGATACATTTACTTAATTTAAATTTAAATTTGGAAGAAATTG 1313
 DB 1306 TTTATTTTACGATCGGAGCATGATATATTTACTTAATTTAAATTTAAATTTGGAAGAAATTG 1365
 QY 1314 ATCGAAGTCAATCAAGCTTATCGTGCATCCAGATTCCTTAAAGTATGATGCTGCTT 1373
 DB 1366 ATCGAAGTCAATCAAGCTTATCGTGCATCCAGATTTAGGATGATGATGCTGCTT 1425
 QY 1374 TTAGAGAAACCAAGTGGATCATGTATTAATTTAGTTTTCCTTATCTCTTATAAATATCTAT 1433
 DB 1426 TTAGAGAAACCAAGTGGATCATGTCAATTTAGTTTAAATAATATCTCTTATAAATATCTGT 1485
 QY 1434 ATATACCTCTTAAACTAAATGCATCTAACACAAATATTAACCTTAGATCTTTAAGA 1493
 DB 1486 CTATCCCTCTTAAACCAATATACATCTAACACAAATATTAACCTTAGATCTTTAAGA 1545
 QY 1494 AATTGCAGAAATTAATGAGGCAAAATAGTCTATGTTGAAGTCTGTTGCTTTC 1546
 DB 1546 AATTGCAGAAATTAATGAGGCAAAATAGTCTATGTTGAAGTCTGTTGCTTTC 1598

AAV52754/c
 ID AAV52754 standard; DNA; 3033 BP.
 AC AAV52754;
 XX
 DT 02-NOV-1998 (first entry)
 XX Nicotiana tabacum osmotin gene with promoter.
 XX
 DE Nicotiana tabacum; tobacco plant; osmotin gene; promoter; inhibition;
 XX fungal pathogen; insect pathogen; nematode pathogen; viral pathogen; ds.
 XX Nicotiana tabacum.
 OS
 XX Key Location/Qualifiers
 FH 2034..2774
 FT CDS /*tag= a
 FT /product= "osmotin"
 FT /transl_except= (pos:2574..2576,aa:Arg)
 XX
 FN US801028-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 07-JUN-1995; 95US-00482037.
 XX
 PR 20-MAY-1993; 93US-00065147.
 PR 12-JAN-1994; 94US-00180428.
 XX
 PA (PURD) PURDUE RES FOUND.
 XX
 XX Hasegawa PM, ; Bressan R;
 XX
 DR WPI; 1998-494773/42.
 DR P-ESDB; AAM69751.
 XX
 PT Inhibition of pathogens in plants by recombinant expression of pathogen
 PT inhibiting proteins - uses nucleic acid constructs containing the
 PT pathogen inhibiting proteins under control of osmotin promoter, which is
 PT inducible by specific signals.
 XX
 PS Claim 1; Col 29-34; 26pp; English.
 XX
 CC A method has been developed of inhibiting a pathogen in a plant. The
 CC method comprises: (a) providing or constructing a vector comprising an
 CC osmotin promoter and foreign DNA sequence encoding a pathogen-inhibiting
 CC protein, where the promoter is operably linked to the foreign DNA
 CC sequence and includes: (i) nucleotide sequence 5' of the osmotin coding
 CC sequence extending to position -248 bases from the start of the osmotin
 CC protein coding sequence, the coding sequence defined as starting at bp
 CC 2034 of the 3033 bp osmotin sequence (present sequence), (ii) a
 CC nucleotide sequence which hybridises to (i) and promotes expression of an
 CC operably linked coding sequence under conditions of desiccation; and (b)
 CC introducing the vector into the plant to create a transformed plant,
 CC where expression of the pathogen-inhibiting protein in the transformed
 CC plant is regulated by the osmotin promoter. The method is useful for the
 CC production of recombinant plants having genes under control of an osmotin
 CC promoter, especially of pathogen inhibiting proteins. Osmotins are
 CC cationic plant proteins, similar to tobacco PR-5-type proteins. The
 CC osmotin genes are under control of hormonal or environmental signals,
 CC including abscisic acid, ethylene, tobacco mosaic virus infection,
 CC salinity, desiccation and wounding. The present sequence represents the
 CC Nicotiana tabacum osmotin gene with promoter
 XX
 SQ Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;
 Query Match 32.3%; Score 500; DB 2; Length 3033;
 Best Local Similarity 71.1%; Pred. No. 7.3e-103;
 Matches 749; Conservative 0; Mismatches 265; Indels 40; Gaps 5;

QY 1 ATCTTTGTTTGAAGAAATTCGAAAGACCTAGGACCACTGGACCTTGGTGCACAAAT 60
 DB 2619 ATCTTTGTTTGAAGAAATTCGAAAGACCTAGGACCACTGGACCTTGGTGCACAAAT 2560

RESULT 5

AAV52754/c

ID AAV52754 standard; DNA; 3033 BP.

61 ATTGTTGTCCTCAAAATGCTGACAGGATTTGTTACATCCTCGGGTACTTTAAGCTGAC 120
 2559 ATTGTTGTCCTCGAATGATAGTACAGGGTTTATTCATCCTCGGAAACCCCTAAGTTCGC 2500
 121 TAGGACATTCACCATTTATATTGCGGTGCATTTGAATTCGTTGGCATTTCCCTCCACTTG 180
 2499 GGGGACATTCGCGGTTTTATATTAGCGGTACAAATGAATTCGATGGCATTTCCCTCCACTAG 2440
 181 GATTAGTCTGGGCGGAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGTCCACAG 240
 2439 GGTAGTCTGGGCGGAAGTCATCGGAATGTTGAATCCATCAACTAAGAAATGTCCACAG 2380
 241 AATCTAAGTTGTTGAACTGCTCGAGGCGTACTCTCGGCTAGGGTGTGTTGCGGGTTTACCCC 300
 2379 AATCTAAGTTGTTGAACTGCTCGAGGCGTACTCTCGGCTAGGGTGTGTTGCGGGTTTACCCC 2320
 301 ACCGGTGCATCTGCAGGACACCAACATACACAGTATGACGACGAACTCTTACAGAGAC 360
 2319 ACCGGTGCATCTGCAGGACACCAACATACACAGTATGACGACGAACTCTTACAGAGAC 2260
 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGCCTTAGGGCGCAT 420
 2259 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGCCTTAGGGCGCAT 2200
 421 CAATGACCAACGTTGGCTCGATCGAGACGTCGCGCACCGCTATCGGGGTGATGCTG 480
 2199 TGATCACCACCAAGTTGGCTCGATCGAGACGTCGCGCACCGCTATCGGGGTGATGCTG 2140
 481 CCAGACGCTGATGACACAGTTGTTGCGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
 2139 CCAGACGCTGATGACACAGTTGTTGCGTACCTCGATAGTGGCAGCATAGTGAAGTCA 2080
 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCATGTTGTTGAAATTT 600
 2079 CCAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGGCCATGTTGTTGAAATTT 2020
 601 ATATGTCGACAAATATATTTTTCGTACT-----TTATATATAGGAT 641
 2019 TTTTAAACAGTTGGGTGTTGCGATATAGTGAACAAATGTTAGTGGTATATAGGGA 1960
 642 ATGGCGGCTTTGGCAGTATGATATTAATCGTATTTATATAAATATCATATCTTTGACT 701
 1959 ATGGCGGCTTTGGCAGTATGATATTAATCGTATTTATATAAATATCATATCTTTGACT 1905
 702 AATTATAACAAATATATATCAATATGATTTGTTAAAGTTGAGTGGC-AAAATGAT 760
 1904 A---ATAACGGATATATCTCAAGGATGCTTTGGCAAGATGGAGCGCGCTTAAACAT 1848
 761 AAGAGCGGCTTAATTAATTAATTTTATGATATAGTATAGTTACAGTGAACCTTTA 820
 1847 AAGAGCGGCTTAATTAATTAATTTTATGATATAGTATAGTTACAGTGAACCTTTA 1800
 821 TTTGTTGATTAACCTTGGACATATAAACTCTGTATCTGTGACGGAACCTTTTCTTAAACTAAA 880
 1799 TTTGTTGATTAACCTTGGACATATAAACTCTGTATCTGTGACGGAACCTTTTCTTAAACTAAA 1740
 881 TATTAAAGAGAGCTATTTTAAATATTTTCGTGGCCAAAGTTTCTTGATATCTATCTAT 940
 1739 AGTCAATTTCTGCTTCTTTTATCTATACCATTTTAAATTTTCGCAAGAAATTTGACAGAT 1680
 941 GCCCATTTTACTTTTATCGTTCTAGCCCTTCTAGGTAGCGGTTTGAACATAAAATCAT 1000
 1679 AGCCACTTTTTCGAGATAGCCATCATTTTAAAGCTATTCATATTTAGTTTATATGTTG 1620
 1001 AAAAATTGAAGTAAAAATTTAGTTTCTTCTAT 1034
 1619 AAAATAAACTCAAAACAAATATATTCGTCACAAA 1586

XX AAX16340;
 AC XX
 DT 26-APR-1999 (first entry)
 XX XX
 DE Tobacco osmotin gene and non-transcribed 5' flanking sequence.
 XX XX
 KW Nicotiana tabacum; tobacco; osmotin; promoter; ds.
 XX XX
 OS Nicotiana tabacum.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 2034..2774
 FT /*tag= a
 FT /transl_except= (pos:2574..aa:Arg)
 XX XX
 FN US5874626-A.
 XX XX
 PD 23-FEB-1999.
 XX XX
 PF 12-JAN-1994; 94US-00180428.
 XX XX
 PR 20-MAY-1993; 93US-00065147.
 XX XX
 PA (PURD) PURDUE RES FOUND.
 XX XX
 PI Hasegawa PM, Bressan R;
 XX XX
 DR WPI; 1999-180080/15.
 DR P-PSDB; AAW94510.
 XX XX
 PT Tobacco osmotin gene promoter - and recombinant construct comprising
 PT foreign gene under its control.
 XX XX
 PS Claim 1; Fig 9A; 26pp; English.
 XX XX
 CC The present sequence represents the DNA sequence comprising the Nicotiana
 CC tabacum (tobacco) osmotin gene and non-transcribed 5' flanking (promoter)
 CC sequence. The present invention specifically claims a DNA fragment
 CC comprising the osmotin gene promoter sequence with no more than 100 bp of
 CC the coding sequence. Also described are methods which are useful in
 CC processes for achieving expression of a coding sequence from a foreign
 CC gene in a host cell
 XX XX
 SQ Sequence 3033 BP; 973 A; 505 C; 547 G; 1008 T; 0 U; 0 Other;
 Query Match 32.3%; Score 500; DB 2; Length 3033;
 Best Local Similarity 71.1%; Pred. No. 7.3e-103;
 Matches 749; Conservative 0; Mismatches 265; Indels 40; Gaps 5;
 Qy 1 ATCTTTGTTGAAAAAATTGAAAAAGACGTAGGACCAATGACCTTGGTGCACAAAT 60
 Db 2619 ATCTTTGTTGAAAAAATTGAAAAAATGTAGGACCAAGTCTTGTGTGCAACAAT 2560
 Qy 61 ATTGTCCTCCCAATGTGTGTAAGGATTTACATCTCCGGGTACTTTAAGCTGAC 120
 Db 2559 ATTGTCCTCCCAATGTGTGTAAGGATTTACATCTCCGGGTACTTTAAGCTGAC 2500
 Qy 121 TAGGACATTCACCAATTTATATTTGTCCTGCAATGAAITGGGTGGCAATTCCTCCACTTG 180
 Db 2499 GGGGACATTCGCGCTTTATATTAGCCGTACAAATGATGCAATTCCTCCACTAG 2440
 Qy 181 GATTAGTCGGGGCAAGATCATCGGTATATTAATCCATCAATGAAGAAATGCCAGA 240
 Db 2439 GGTAGTCGGGGCAAGATCATCGGTATATTAATCCATCAATGAAGAAATGCCAGA 2380
 Qy 241 AATCTAAGTTGTTGAATCTGTCGAGCGGTACTCGGTAGGGTGTGTCGGGTATACCCC 300
 Db 2379 AATCTAAGTTGTTGAATCTGTCGAGCGGTACTCGGTAGGGTGTGTCGGGTATACCCC 2320
 Qy 301 ACCCGGTGCACTGAGGACACCAACCAATCAGCAGTCATGACGAACTCTACCAAGCAC 360
 Db 2319 ACCCGGTGCACTGAGGACACCAACCAATCAGCAGTCATGACGAACTCTACCAAGCAC 2260

Qy 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTCCTAGGCCAT 420
 Db 2259 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTCCTAGGCCAT 2200
 Qy 421 CAATGACCCACGTTTGGCTCGATCGAGACCTCGGCCACCGCCTATCGGGGTCCATGCTG 480
 Db 2199 TGATCACCACCAAGTTTGGCTCGATCGAGACCGCCGCCACCGCCTATGGGTGTCACGCCG 2140
 Qy 481 CCCAGACGGTGTATGGACAGTTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
 Db 2139 CCCAAACGGTGTACGGACAGTTTGGACCTCGATAGTGGCAGCATAGTGAAGTCA 2080
 Qy 541 CAAAAGCAAGAGGAGGAAGAAACAAAGAAATCTCAAGTAGGCCCATGTTTGTTCGAAATTT 600
 Db 2079 CCAAGGCAAGGAGGAGGAAGAAACAAAGAAATCTCAAGTTGCCCATGTTTGTTCGACATTT 2020
 Qy 601 ATATGTGGACAAATTAATTTTGGTACT-----TTATATATAGGGAT 641
 Db 2019 TTTTAAACAAGTTGGTGTGGATATAGTACAAATTTGTTAGTGGTTTATATAGCGGA 1960
 Qy 642 ATGGCGGCTTTTGGCACTATCGATATTAATCGTATTATATAACAATATCATCTTTCAT 701
 Db 1959 ATGGCGGCTTTTGGCACTATCGATATTAATC-----ATAAATATTATTATCATCTTTCAT 1905
 Qy 702 AATTATAAAACAAATAATATTACAATATGATTTGGTAAACGTTGAGGTGGC-AAAATGTAT 760
 Db 1904 A-----ATAAACGGATATATCTCAAGATGCTTTGGCAAGATGGAGCGCGCTTAAACAT 1848
 Qy 761 AAGAGCCGCTTAATAATTAATTTATGAAATATAGACTATAGTTTACAAGTGAACTTTA 820
 Db 1847 AAGAGCCGCTTAATAATTAATTTATGAAATATAG-----AAGTCAATTTA 1800
 Qy 821 TTTGGTGATAACTTGGACATATAAACTCTGATCGTGACGGAAGTCTTCTTAAACATAAA 880
 Db 1799 TTTGGTAATAAGCTGACCTATATCTCTGPAAGTGACACTTGTACAATATCTCTTT 1740
 Qy 881 TATTAATAAGCAGCTATTTTAATATTTTCTGGCCAAAGTTTCTTGCATACCTTATCTAT 940
 Db 1739 AGTCAATTTCTGCTTCTTTTATCTATACCAATTTTAAATTCGCAAGAAATTCACAGAT 1680
 Qy 941 GCCCATTTTACTTTTATCGTTCTAGCCTTCTAGGTAGCGGTTTGAACATAAAATCAT 1000
 Db 1679 AGCCACCTTTTGGCAGATAGCCATCTTTAAAGCTATTTCAATATTTAGTTTTTAATGTG 1620
 Qy 1001 AAAAATCGAAAGTAAAAATTAGTTTTTTTTCATA 1034
 Db 1619 AAAATAAAACTCAAAACAATATATTCTGTCACAAA 1586
 ID AAQ15269 standard; cDNA; 883 BP.
 XX AC AAQ15269;
 XX AC
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1992 (first entry)
 XX XX
 DE Osmotin-like antifungal protein.
 XX XX
 KW tobacco; osmotic tolerance; ss.
 XX XX
 OS Nicotiana tabacum.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 17..757
 FT /*tag= a
 FT /note= "osmotin-like"
 XX XX
 FN EP460753-A.
 XX XX
 PD 11-DEC-1991.

241 AATCTAAGTTGTTGAACCTGGTCCGAGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 300
 362 AATCTAACCACCTGAATTGGTCCAAAGCGTATTACGCAAGGTGTTTGGTGGTTTACCCC 303
 301 ACCCGGTGCACTGACGACACACCAACATCCACAGTCATGACGACCACTCTACGAGCAC 360
 302 ACCCGGTGCACTGACGACCTCCACACAGTCATGACGACCACTCTACGAGCAC 343
 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCTAGTGCCTAGGCGGCAT 420
 242 CATTTGAAGTTACATTTAGTACGGCCCATACAGTGCATTTTAGTACCTCGTGGCGCAT 183
 421 CAATGACCCACGTTTGGCTCGATCGACAGCGTTCGGCCACCGCTATCGGGGTGCTGCTG 480
 182 TGATCAACCCAGTTTGGCTCGATCGACAGCGTTCGGCCACCGCTATCGGGGTGCTGACGCG 123
 481 CCCAGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
 122 CCCAAGCGGTGTACGGACAGTTGTTCCGACCTCGATAGTGGCAGCATAGTGAAGTCA 63
 541 CAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTACGCCATGT 588
 62 CCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTACGCCATGT 15

RESULT 8

AAV68641/c
 ID AAV68641 standard; DNA; 741 BP.

AC AAV68641;

DT 12-MAR-1999 (first entry)

Nucleotide sequence of the osmotin AP24.

Osmotin AP24; beta-(1,6)-glucanase; bG; chimeric DNA;
 anti-fungal composition; transgenic plant; pathogen resistant; ds.
 Nicotiana tabacum.

Key Location/Qualifiers
 FT 1..741
 CDS /tag= a
 FT /product= "osmotin AP24"

XX WO9849331-A1.

XX 05-NOV-1998.

XX 27-APR-1998; 98WO-EP002580.

XX 29-APR-1997; 97EP-00201254.

XX (MOGE-) MOGEN INT NV.

XX Stuiver MH, Lageweg W, Van Deventer- Troost JPE, Custers JHHV;

XX WPI; 1999-024066/02.

XX P-PSDB; AAW80986.

XX Isolated protein with beta-glucanase activity - is isolated from edible fungus and used to produce pathogen resistant plants.

PS Claim 13; Page 27-28; 47pp; English.

CC This is the nucleotide sequence encoding the Nicotiana tabacum osmotin
 CC AP24, used in the method of the invention in conjunction with beta-(1,6)-
 CC glucanase (bG) to produce a chimeric DNA. Osmotin AP24 and beta-(1,6)-
 CC glucanase (bG) can be used in an anti-fungal composition. The chimeric
 CC DNA sequences can be transferred into plants to make them pathogen
 CC resistant

SQ Sequence 741 BP; 182 A; 173 C; 178 G; 208 T; 0 U; 0 Other;
 Query Match 29.0%; Score 448.4; DB 2; Length 741;
 Best Local Similarity 85.3%; Pred. No. 2.1e-91;
 Matches 500; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 QY 1 ATCTTGTGTTTCGAAAGAAATGGAAGAAAGCGTAGGACACATGGACCTTGGGTGCAACAAT 60
 DB 586 ATCTTGTGTTTCGAAAGAAATTTGAGAAATTTAGAACCCACAGGTCCTTGTGTGCAACAAT 527
 QY 61 ATTGTGTGCTCCCAATGTGTACAGGATTTTACATCTCTCCGGGACTTTTAAGCTGAC 120
 DB 526 ATTGTGTGCTCCCAATGTGTACAGGATTTTACATCTCTCCGGGAAACCTTAAGTTGCG 467
 QY 121 TAGGACATTCACCATTTATTTCCCGTGCATTCGAATTTGCTGGCATTTCCCTCCACTTG 180
 DB 466 GGGGACATTCCTCCCGTTTATATTAGCCGTACAAATGAATTTGCATGGCATTTCCCTCCACTAG 407
 QY 181 GATTAGTCGGGGCGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCCAGA 240
 DB 406 GGTTAGTCGGGGCGAAAGTCATCGGAATTTGAATCCATCAACTAAAGAAATGTCCAGA 347
 QY 241 AATCTAAGTTGTTGAACCTGGTCCGAGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 300
 DB 346 AATCTAAGTTGTTGAACCTGGTCCGAGCGTACTCGGCTAGGGTGTGTTGGCGGTTTACCCC 287
 QY 301 ACCCGGTGCACTGACGACACACCAATCCACAGTCATGACGAAACCTCTACGAGCAC 360
 DB 286 ACCCGGTGCACTGACGACCTCCACCAAGTCACCGGTTTGGCAGCTACCCCTACGAGCAC 227
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTACGCTAGTGCCTAGGCGCAT 420
 DB 226 CATCGAAGTTACATTTAGTACGGCCCATACACGTCGCAATTTTAGTACCTCTGTCGCGCAT 167
 QY 421 CAATGACCCACGTTTGGCTCGATCGACAGCGTTCGGCCACCGCTATCGGGGTGCTGCTG 480
 DB 166 TGATCAACCCAGTTTGGCTCGATCGACAGCGTTCGGCCACCGCTATCGGGGTGCTGACGCG 107
 QY 481 CCCAGACGGTGTATGGACAGTTTGGTTCGCTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
 DB 106 CCCAAGCGGTGTACGACAGTTGTTTCGACCTCGATAGTGGCAGCATAGTGAAGTCA 47
 QY 541 CAAAGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTACGCCAT 586
 DB 46 CCAAGGCAAGGAGGAGGAGAAACAAAGAGATCTCAAGTACGCCAT 1

RESULT 9

AAQ21414/c
 ID AAQ21414 standard; DNA; 1004 BP.

XX AC AAQ21414;

XX 10-JUN-1992 (first entry)

XX Encodes osmotin-like protein from tobacco plant.

XX drought tolerance; salt tolerance; environmental stress; ss.

XX Nicotiana tabacum.

XX Key Location/Qualifiers

FT sig_peptide 18..80

FT /tag= a

FT mat_peptide 81..773

FT /tag= b

FT /product= "osmotin_like_protein"

XX JP04018099-A.

XX 22-JAN-1992.

XX 10-MAY-1990; 90JP-00121816.

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XX 10-MAY-1990; 90JP-00121816.
XX (NAGS ) NAGASE SANGYO KK.
XX WPI; 1992-075255/10.
XX P-PSDB; AAR21426.
XX Amino-acid sequence for protein resembling osmotic - for prodn. of higher
XX plants resistant to stress such as drought, salt etc.
XX Claim 3; Fig 1; 10pp; Japanese.
XX The protein encoded by this DNA is an osmotin-like protein involved in
XX resistance to stress in higher plants. Stress may be caused by e.g. viral
XX infection, drought, high salt concentration, etc. See also AAQ21415-8
XX
XX Query Match 24.7%; Score 382.2; DB 2; Length 1004;
XX Best Local Similarity 78.3%; Pred. No. 2.1e-76;
XX Matches 472; Conservative 0; Mismatches 128; Indels 3; Gaps 1;
XX
QY 1 ATCTTTGTTGAAAATAATGGAAGAAGACGTAGGACCATGGACCTTGGGTGCAACAAT 60
Db 606 ATCTTTGTTGAAACCATCTTGATAACTCAGTAGGACCATGGTCCCTTGTTGCAACAAT 547
QY 61 ATTGTGTCTCCCAATGTGTACAGGATTTGTACATCTCCCGGTACTTTAAGCTGAC 120
Db 546 ATTGTGTCTCCCAATGTGTACAGGATTTGTACATCTCCCGGTACTTTAAGCTGAC 487
QY 121 TAGGACATTCACCAATTTATTTGGCGTGCAATGAATTTGGTGGCAATTCCTCCACTTG 180
Db 486 CAGGCATTCACCAATTTATTTGGCTGTGCAATGAATTTGGTGGCAATTCCTCCACTTG 427
QY 181 GATTAGTCGGGGGAAAGTATTCGGTATTTAAATTCATCAATCAATCAATCAATCAATCAAT 240
Db 426 GCTTAGTCGGGGGAAAGTATTTAAATTCATCAATCAATCAATCAATCAATCAATCAATCAAT 367
QY 241 AATCTAGTCTTGAATGTTCCGAGGCGTACTCGGCTAGGCTTTGGCGGTTTACCC 300
Db 366 AATCTAGTCTTGAATGTTCCGAGGCGTACTCGGCTAGGCTTTGGCGGTTTACCC 307
QY 301 ACCCGGTGCACTGAGGACACCAACAATCACCAGTCAATGACGAACTCTACAGCAC 360
Db 306 ATCTTTGCAATTAAGACTTCACCAACAATCACCAGTTCGACCACTCTACAGCAC 247
QY 361 CATGAGATTACATCCAGTACGACCCCATATACGTGCGCATGTAGTCCCTTAGGCGCAT 420
Db 246 CATCAAGTTGCAATTAAGTACGACCCCATATACGTGCGCATTTTAGTACAGGTTGCGCC 187
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGCGGCAACCGCTATCGGGTGTGATGCTG 480
Db 186 AGAACCCCACTTTGACCTGTTGAGACGTGCGGCAACCGCTATCGGGTGTGCGCTG 127
QY 481 CCCAGAGGTGTATGAGAGTGTGCGTACCTC---GATGTGGCAGCATAGTGAAG 537
Db 126 CCCAGAGGTGTATGAGAGTGTGCGTACCTC---GATGTGGCAGCATAGTGAAG 67
QY 538 TCACAAAGCAAGAGGAGGAGAAACAAGAGATCTCAAGTAGCCATGTTTGTGAAA 597
Db 66 TCACAAAGCAAGAGGAGGAGAAACAAGAGATCTCAAGTAGCCATGTTTGTGAACT 7
QY 598 TTT 600
Db 6 TTT 4

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RESULT 10
AAC47993/c
ID AAC47993 standard; DNA; 906 BP.
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AC AAC47993;

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XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 55872.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
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XX 08-JUN-1999; 99US-0137502P.
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XX 18-JUN-1999; 99US-0139454P.
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XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
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XX 18-JUN-1999; 99US-0139463P.

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PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
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Query Match 13.5%; Score 208.2; DB 3; Length 906;

Best Local Similarity 62.8%; Pred. No. 3.8e-37;

Matches 381; Conservative 0; Mismatches 208; Indels 18; Gaps 3;

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QY 55 AACAATATGTTGCTCCTCCAATGTTGACAGGATTTGTTACCTCTCCGGGTACTTTAA 114

Db 556 AACAGTATTTGGTTTCGCTGGAATACAGTACACGGGTTTTCATCCACCTGGGCTCTCA 497

QY 115 GCTGACTAGGACATTCACCATTTATTTGCGGTGCAATGTAATTCGTTGGCAATTCCTC 174

Db 496 ACACGTTTGGACATTTGTCGTTTATGTTCTGCGGTACATAGTATCGATGCGATGGCAGTTC---- 441

QY 175 CACTTGGATTAGTCGGGGGGAAGTCATCGGTATATTAATCCCACTCAACTAAAGATGT 234

Db 440 -----GAACCTAGTTGGGTAACTCCATAGGTATGTTAAATCCATCGAAGTGAATAT 386

QY 235 CCCAGAAATCTAAGTTGTTGAACTCGTCCGAGCGCTACTCGGTAGGTGTTTGGCGGTT 294

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Db      385 CGTAGAGTCTAAGTTGTTGAATGTTCAAGCGTACTCAGCCAACTGTTGGTGGGT 326
QY      295 TACCCACCCCGGTGCACCTGCAGGACACCAACCAATCACCAGTCTATGACGAACTCTTAC 354
Db      325 GTCCCCAGCCAGTACATTGGAGTCCACCACTGCAGTCCAGTCTGGCATCGGCCACGAC 266
QY      355 CAGCACCATCGAAGTTACATCCAGTACGACGCCCATATAGTGCCTATCGTGGCTCG 414
Db      265 CTGAGAGTCAAGTTTCAATTTGGTCTTACCCCAATCCGTGCCATTTAGTGGCCCGCG 206
QY      415 GGCATCAATGACCCACACCTTTGGCTTCGATCGAGACGTCCGCCACCGCTATCGGGGTG 474
Db      205 CGACATCTAGCTCCATGATTTGGCCAGCATCTAGAGGTGGCCACCTCC---AGGGCTTG 149
QY      475 ATGCTGCCAGACGCTGTATGGACAGTTGTTGCGTACCTCGATAGTGCACGACATAAGTGA 534
Db      148 CGCGAGCCCAACACCGGTGTAACTACATTCGTTTAGGATTTCAATGTGGCGCTGTTGGG 89
QY      535 AAGTCACAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGTG 594
Db      88 TGGAGATGAGCAAAAGTCCGGAATAATGAAAGTAGACCAAGAGTTTCCCATTTTTT 29
QY      595 AAATTTA 601
Db      28 AGTTCTA 22

RESULT 11
AAC47227/c
ID AAC47227 standard; DNA; 902 BP.
XX
AC AAC47227;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53029.
XX
XX Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP:033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 29-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 08-APR-1999; 99US-0128234P.
XX 16-APR-1999; 99US-0128714P.
XX 19-APR-1999; 99US-0129845P.
XX 21-APR-1999; 99US-0130077P.
XX 23-APR-1999; 99US-0130449P.
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XX 28-APR-1999; 99US-0130891P.
XX 30-APR-1999; 99US-0131449P.
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XX 04-MAY-1999; 99US-0132407P.
XX 05-MAY-1999; 99US-0132484P.
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XX 07-MAY-1999; 99US-0132487P.
XX 11-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
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XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
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XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
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XX 10-JUN-1999; 99US-0138540P.
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PR 23-JUL-1999; 99US-0145224P.
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PR 29-SEP-1999; 99US-0156596P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 13.4%; Score 207.8; DB 3; Length 902;
Best Local Similarity 63.5%; Pred. No. 4.7e-37;
Matches 355; Conservative 0; Mismatches 192; Indels 12; Gaps 2;

QY 43 GACCTTGGGTGCAACAATATTGTTGCTCCTCAAAATGGGTACAAGGATTGTTACATCTC 102
DB 564 GACCTTGGTACCAACAGTATTGGTCTGTAATACAGTACACGGTGTGTCATCCAC 505
QY 103 CGGGTACTTTAAGCTGACTAGGACATTCACCATTTATATTTTCCCGTGCAATGAAATGCGT 162
DB 504 CTGGGGCTCTCAACACGTTTGGACATTTGTCGTTATGTCGCGGTACATAGTATCCGAT 445
QY 163 GGCATTTCCCTCCACTTCGATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAA 222
DB 444 GGCAGTTC-----GAAGTGTGGGCTAAACTCCATAGGTATGTTAAATCCATCGA 394
QY 223 CTAAAGAAATGTCCAGAAATCTAAGTTGTTGAACTGGTCCGAGGCGTACTCGGCTAGGG 282
DB 393 CAAGTGAGTATCGTAGAGTCTAAGTTGTTGAATTTGTTCAAAGCGTACTCAGCCAACG 334
QY 283 TGTGTTGGCGTTTACCCACCGGTGCACTCGAGGACACCAACCAATCACCAGTCATGC 342
DB 333 TGTGTTGGTGGTGTCTCCAGCCAGTACATTGGAGTCCCACTCGAGTCACCGTTGGC 274
QY 343 ACGAACTCTTACCAAGCACCATCGAAGTTACATCCAGTACGACCCCAATATAGTCCATCG 402
DB 273 ATCGGCCAGACCTGAGAGTCAAGTTACATTTGTTCTTACCCCAATCGTGCCATTT 214
QY 403 TAGTGCCCTTAGCGGCATCAATGACCCACGTTTGGCTCGATCGAGAGCTCGGCCACCGC 462
DB 213 TAGTGCCCGCGGACATCTAGCCTCCATGATGGCCAGCATCTAGAGCTCGGCCACCTC 154
QY 463 CTATCGGGTGCATGCTGCCAGCGGTGATGGACAGTTGTTGCTACCTCGATAGTGG 522
DB 153 C---AGGGCTTGGCGCAGCCCAACGCGGTGTAACATGTTGGTTTAGGATTTGGAATG 97
QY 523 CAGCATAAAGTGAAGTCAAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGC 582
DB 96 CGGCTGTTGCGGTGGAGATGAGCAAAAGTGGGAAATATGAAAGTAGAGACCAAGAGGT 37
QY 583 CCATGTTTGTGAATTTA 601
DB 36 TTGCCATTTTGTAGTTCTA 18

RESULT 12
AB214313/c
ID AB214313 standard; DNA; 735 BP.
XX
AC AB214313;
XX
XX
XX 21-JAN-2003 (first entry)
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2118.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
XX
XX
XX WO200216655-A2.
XX
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28-FEB-2002.

24-AUG-2001; 2001WO-US026685.
24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
(SCRI) SCRIPPS RES INST.
(SYGN) SYNGENTA PARTICIPATIONS AG.
Harper JF, Kreps J, Wang X, Zhu T;
WPI; 2002-304127/34.
Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
Claim 144; SEQ ID NO 2118; 577pp + Sequence Listing; English.
The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention. Note: the sequence data for this patent is
not represented in the printed specification but is based on sequence
information supplied to Derwent by the European Patent Office
Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

Query Match 13.4%; Score 207.2; DB 6; Length 735;
Best Local Similarity 64.16%; Fred. No. 6.1e-37;
Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2

QY 43 GACCTTGGGTGCAACAATATTGTTCCTCCAAATGGTGACAGGAATGTTACATCCTC 102
DB 535 GACCCTTCGTACACAGTATTGGTTCGTCTGAATACAGTACACGGGTGTTGCATCCAC 476
QY 103 CGGTGACTTTAAGCTGATAGACATTCACATTTATAATTGCGGTGCAATTGAATTGGT 162
DB 475 CTGGGGCTCTCAACACGTTTGGCATTTGCCGTTTATGCTGGGTGACATAGTAGTCCGAT 416
QY 163 GCATTTTCCTCCACTTCGATTAGTTCGGGGCGAAGTCATCGGTATTAATAATCCATCAA 222
DB 415 GGCAGTTC-----GACTAGTTGGCTAACTCCAATAGTATGTTAATTCATCA 365
QY 223 CTAAAGAAATGCCAGAAAATCTAAGTTGTTGAACCTGGTCCGAGGCGTACTCGGTGAGG 282
DB 364 CAAGTGAGATATCGTAGAAGCTAAGTTGTTGAATTTGGTTTCAAAGCGTACTCAGCCACG 305
QY 283 TGTTTTGGGGTTTACCCACCGGTGCACTGCGAGCACACACCAATCACCAGTCACTGC 342
DB 304 TGTTTTGGGTGCTGCTCCCAGCCAGTACATTGGAGTCCACCACCTGCAGTACCAGTTGGC 245
QY 343 ACAGAACCTCTACCGACACCATCGAAGTTTACATCCAGTACGACCCCCATATACGTGCCATCG 402
DB 244 ATCGGCCACGACCTCGAGGAGTCAAAGTTACAAATTTGGTCTTACCCCAATCCGTGCCATT 185
QY 403 TAGTGCCCTTAGCGCATCAATGACCCACGTTTGGCTCGATCGACAGCTCGGCACCGC 462
DB 184 TAGTGCCCGCGCGCATCTTAGCTCCCATGATTTGGCCAGCATCTAGACGTGCGGCCACCTC 125
QY 463 CTATCGGGGTTCGATCGTCCACAGACGGGTGATGACAGTGTGTCGCTACTCGATAGTGG 522
DB 124 C---AGGGCTTCGCGCACCCACACGGGTGTACTACATTTGGTTTAGATTTGCAATGGG 68
QY 523 CAGCATATAGTGAATGTCACAAAACAGAGAGGGAGAAAAACAAAGAAGATCTCAAG 578

Db 67 CGGCTGTTCGGTGGAGATGACCAAAAGTCCGGAATATGAAAGTAGAGACCAAG 12

RESULT 13
ABZ42096/c

ID ABZ42096 standard; cDNA; 735 BP.

XX XX

AC ABZ42096;

XX XX

DT 27-FEB-2003 (first entry)

XX XX

DE Arabidopsis thaliana gene #80 modulated by PTGS.

XX XX

KW Poetranscriptional gene silencing; PTGS; plant; transformation; gene;

KW ss.

XX XX

OS Arabidopsis thaliana.

XX XX

Key Location/Qualifiers

XX FH 1. 735

CDS /*tag= a

FT FT

XX XX

PN W0200281595-A2.

XX XX

PD 17-OCT-2002.

XX XX

XX 05-APR-2002; 2002WO-EP003806.

XX XX

PR 06-APR-2001; 2001US-0282049P.

XX XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PA (FRIE-) FRIEDRICH MIESCHER INST.

XX XX

PI Zhu T, Glazov EA, Meins F, Wang X, Chang H;

XX XX

XX WPI; 2003-103337/09.

DR DR

DR P-PSDB; ABP81252.

XX XX

PT Novel polynucleic acid segment useful for modulating gene expression

FT within a cell by posttranscriptional gene silencing, and for augmenting a

PT plant cell genome.

XX XX

PS Claim 18; Page 324-325; 438pp; English.

XX XX

CC The invention relates to a novel isolated polynucleic acid segment

CC modulated within a cell by posttranscriptional gene silencing (PTGS). The

CC invention specifically relates to a method to identify an expression

CC product that is modulated by PTGS. The polynucleotide is useful for

CC modulating the gene expression within a cell by PTGS, by introducing the

CC polynucleic acid into a cell and expressing the nucleic acid segment in

CC the cell to form a product. The polynucleic acid segment is also useful

CC for augmenting a cell genome, and for augmenting a plant genome, by

CC contacting a plant cell with the segment to produce a transformed plant

CC cell, and growing the transformed plant cell to produce a differentiated

CC transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent

CC segments of A. thaliana cDNA modulated by PTGS

XX XX

SQ Sequence 735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;

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	Best Local Similarity	64.6%	Pred. No. 6.1e-37		
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Qy	43	GACCTTGGGTGCAACAATATTTGTCCTCCAAATGTTGTTACAGGATTTGTTACATCTC	102		
Db	535	GACCGTTCGTACACACGATATTGGTTCGTGAAATACAGTACACGGGTGTTGTCATCCAC	476		
Qy	103	CGGGTACTTTAAGTGTACTAGGACATTCCACATTTATATTTCGCGTGCATTTGGAATTTGGGT	162		
Db	475	CTGGGGCTCTCAACACGGTTTGGACATTGTCCGTTTATGTCTGCGGTACATAGTATCCGAT	416		
Qy	163	GGCATTTCCCTCCACTTGGATTTAGTCGGGGGAAAGTCATCGGTATATTAAATCGATCAA	222		

Db	415	GGCAGTTC-----GAACTAGTTGGGCTAAACTCCTATAGTATGTTAAATCCCATCGA	365
Qy	223	CTAAAGAAATGTCCAGAAATCTAAGTTTGTAACTGGTCCGAGGGCTACTCGGCTTAGGG	282
Db	364	CAAGTCAGATATCGTAGAAGTCTAAGTTGTGTGAATTGGTTCAAAGCGTACTCAGCCAAAG	305
Qy	283	TGTTTGGCGGTTTACCCACCCGGTGCATCTCAGGACACCCACCAATCACCAGTCAATCG	342
Db	304	TGTTTGGTGGCTGTCCCAGCCAGTACATTGGAGTCCACCACCTGCAGTACCAAGTTTGGC	245
Qy	343	ACGAACCTCTTACCAGCACCATCGAAGTTTACATCCAGTACGACCCCATATATACGTGCCATCG	402
Db	244	ATCGGCCACAGCCTGAGGAGTCAAAGTTTACAAATTTGGTCTTACCCCAAATCCGTGCCATT	185
Qy	403	TAGTGGCCCTAGGCGCATCATGACCCACCTGGTGGCCTCGATCGAGACGTCGGCCACCGC	462
Db	184	TAGTGGCCCGCCGACATCTAGCTCCATGATTGGCCAGCATCTAGACGTCGGCCACCTC	125
Qy	463	CTATCGGGTCGATCTCCAGACGGTGTATGCACAGTTGTTTGGCTACCTCGATATGCG	522
Db	124	C---AGGGCTTCGGCGACCCACACGGGTGTAATACATTCATTGGTTTAGGATTTGCAATGTGG	68
Qy	523	CAGCATAGTGAAGTCAAAAGCAGAGGGAGAAAACAAAGAGATCTCAAG	578
Db	67	CGGCTGTTCGGTGGAGTAGACAAAAGTCCGGAATAATGAAGTAGAGACCAAG	12
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AC	ADA68525;		
XX			
DT	20-NOV-2003 (first entry)		
XX			
DE	Arabidopsis thaliana gene, SEQ ID 566.		
XX			
KW	Plant; bacterial infection; fungal infection; viral infection; ds.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	WO2003000899-A1.		
XX			
PD	03-JAN-2003.		

XX	SQ	Sequence	735 BP; 192 A; 192 C; 173 G; 178 T; 0 U; 0 Other;
		Query Match	13.4%; Score 207.2; DB 7; Length 735;
		Best Local Similarity	64.6%; Pred. No. 6.1e-37;
		Matches	346; Conservative
			0; Mismatches 178; Indels 12; Gaps 2
Qy	43	GACCTTGGGTGCAACAATATTGTTGTCTCCAAATGGGTACAGAGNATGTTTACATCCCTC	102
Db	535	GACCGTCTGTACAAACAGTATTGGTTGGTCTGAAATACAGTACACGGGTGTTGTCCATCCAC	476
Qy	103	CGGGTACTTTAAGCTGATAGAGCAATTCACCATTTATATTGGTCGTGCATTTGAATTTGCGT	162
Db	475	CTGGGGCTCTCAACACGTTTGACATTTGTCGGTTATGTTCTGCGGTACATAGTATCCGAT	416
Qy	163	GGCATTTCCCTCCACTTCGGATTAGTCGGGGCGGAAAGTCATCGGTATATTTAAATCCATCAA	222
Db	415	GGCAGTTC-----GAACTAGTTGGGGCTAAACTCCATAGATGATGTTAAATTCATCGA	365
Qy	223	CTAAGAANAATGTCACAGAAATCTAAGTTGTTTGAACCTGGTCGAGGCGGTACTCGGCTAGGG	282
Db	364	CAAGTGAGATATCGTAGAAGCTTAAGTTGTTTGAATTTGGTTCAAAGCGTACTCAGCCCAAG	305
Qy	283	TGTTTGGCGGTTTACCCACCGGTTGACATGCAAGCAACCAACCAATACACAGTCATCGC	342
Db	304	TGTTTGGTGGCTGTGTCGCCAGGCAGTACATTGGAGTCCACCACCTGCAGTCACCAAGTTTGGC	245
Qy	343	ACGAACCTCTACACGACCATTCGAAGTTTACATCCAGTACGACCCCATATACGTGCCATCG	402
Db	244	ATCGGCCACGACTGAGGAGTCAAAGTTTACATTTGGTCTTACCCCAATCCGTGCCATTT	185
Qy	403	TAGTGCCTCTAGCGGCATCAATGACCCACGTTTGGCTTCGATCGAGACGTCGGGCCACCGC	462
Db	184	TAGTGCCTCCCGCAGCATCTAGCCTTCCATGATTTGGCCAGCATCTAGACGTCGGGCCACCTC	125
Qy	463	CTATCGGGGTCCGATCCTCCACAGCGGTGTATGACACAGTTTGTTCGTCCTCGATATGTCG	522
Db	124	C---AGGGCTTCGGCGACCCACACGGTGTAACTACATTTGGTTTGAAGTTTCGATTTGG	68
Qy	523	CAGCATTAAGTGAAGTCTCAAAAACAAGAGGGGAGAAAAAATAAAGAGATCTCTCAAG	578
Db	67	CGGCTGTTTTCGGGTGAGATGAGCAAAAGTCGCGAAAAATATGAAAGTAGAGACCAAG	12

PA (YUY/) YU Y.
 PA (NAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI; 2002-403163/43.
 XX
 PT New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 PT producing compositions that modulate the expression or function of its
 PT encoded protein, and mapping functional regions of protein.
 XX
 PS Claim 1; SEQ ID NO 334; 49pp + Sequence Listing; English.
 XX
 CC The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful for
 CC enhancing or inhibiting production of a biosynthetic product in a plant.
 CC (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=99909770445
 XX
 SQ Sequence 950 BP; 261 A; 225 C; 213 G; 251 T; 0 U; 0 Other;

Query Match 13.4%; Score 207.2; DB 6; Length 950;
 Best Local Similarity 64.6%; Pred. No. 6.5e-37;
 Matches 346; Conservative 0; Mismatches 178; Indels 12; Gaps 2;
 43 GACCTTGGTGCACAAATATTGTCCTCCAAATGGTACAGAGATTCCTTACATCCTC 102
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 543 GACCGTTCTGTACAAAGATATTGGTTGCTCTGAATACAGTACACAGGGTCTTGCATCCAC 484

Search completed: August 18, 2004, 07:59:11
 Job time : 555.632 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 06:27:01 ; Search time 119.074 Seconds
(without alignments)
7205.239 Million cell updates/sec

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Perfect score: 1546
Sequence: 1 atctttgttgaaaaattg.....tggtgaagtgtgtgttc 1546

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	500	32.3	3033	1	US-08-482-037A-1
C 2	450.4	29.1	883	1	US-07-828-798C-4
C 3	450.4	29.1	883	2	US-08-315-868A-4
C 4	450.4	29.1	883	3	US-08-495-819B-4
C 5	450.4	29.1	884	1	US-07-828-798C-5
C 6	450.4	29.1	884	2	US-08-315-868A-5
C 7	450.4	29.1	884	3	US-08-495-819B-5
C 8	180.6	11.7	875	4	US-08-589-733C-4
C 9	159.2	10.3	900	1	US-08-181-271A-4
C 10	159.2	10.3	900	1	US-08-449-315-4
C 11	159.2	10.3	900	1	US-08-444-803-4
C 12	159.2	10.3	900	1	US-08-449-043-4
C 13	159.2	10.3	900	1	US-08-456-265A-4
C 14	159.2	10.3	900	1	US-08-455-416-4
C 15	159.2	10.3	900	1	US-08-455-244-4
C 16	159.2	10.3	900	1	US-08-454-876-4
C 17	159.2	10.3	900	2	US-08-457-364-4
C 18	159.2	10.3	900	2	US-08-456-262-4
C 19	159.2	10.3	900	2	US-08-456-240-4
C 20	159.2	10.3	900	2	US-08-455-736-4
C 21	159.2	10.3	900	2	US-08-971-217-4
C 22	159.2	10.3	900	3	US-09-350-600-4
C 23	159.2	10.3	900	4	US-09-306-234-4
C 24	152.6	9.9	910	4	US-08-685-292-1
C 25	124.8	8.1	894	1	US-08-178-708-7
C 26	124.8	8.1	894	1	US-08-457-552-7
C 27	124.8	8.1	894	1	US-08-456-430-7

C 28	124.8	8.1	894	2	US-08-994-418-7
C 29	124.8	8.1	894	5	PCT-US95-00432-7
C 30	101	6.5	1309	6	5221624-4
C 31	94	6.1	621	4	US-09-224-514A-1
C 32	94	6.1	621	6	5221624-31
C 33	92.8	6.0	621	4	US-09-224-514A-9
C 34	83	5.4	624	2	US-08-426-599B-3
C 35	76.4	4.9	624	2	US-08-426-599B-1
C 36	73.8	4.8	2051	1	US-08-482-037A-2
C 37	67.8	4.4	230	4	US-09-589-733C-28
C 38	52	3.4	636	3	US-08-998-416-1137
C 39	51.6	3.3	832	4	US-09-621-976-2813
C 40	51.2	3.3	6152	3	US-08-973-462-1
C 41	51	3.3	19233	4	US-10-204-708-45
C 42	49.4	3.2	665	2	US-08-883-795A-36
C 43	49.2	3.2	64081	4	US-09-790-988-1
C 44	48.4	3.1	832	4	US-09-621-976-2813
C 45	48.4	3.1	3095	6	5231168-1

ALIGNMENTS

RESULT 1
US-08-482-037A-1/c
; Sequence 1, Application US/08482037A
; Patent No. 5801028
; GENERAL INFORMATION:
; APPLICANT: Ray Bressan and Paul M. Hasegawa
; TITLE OF INVENTION: Csmotin Gene Promoter and Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Q. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204-5137
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,037A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/476,243
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/180,428
FILING DATE: January 12, 1994
APPLICATION NUMBER: 08/065,147
FILING DATE: May 20, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Q. Henry
REGISTRATION NUMBER: 28,309
REFERENCE/DOCKET NUMBER: 7024-8/PUR16CIPDIVII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 634-3456
TELEFAX: (317) 637-7561
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 bases
TYPE: Nucleotide/Amino Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA

US-08-482-037A-1
Query Match 32.3%; Score 500; DB 1; Length 3033;

Best Local Similarity 71.1%; Pred. No. 2.7e-112; Mismatches 265; Indels 40; Gaps 5;
Matches 749; Conservative 0;

Qy 1 ATCTTTGTTTGAATAAATGGAAGAAAGCGTAGGACCATGACCTGGGTGCAACAAT 60
Db 2619 ATCTTTGTTTGAATAAATGGAAGAAAGCGTAGGACCATGACCTGGGTGCAACAAT 2560

Qy 61 ATTGTTGCTCCTCAAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 2559 ATTGTTGCTCCTCAAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 2500

Qy 121 TAGGACATTCACCAATTTATATTTGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTTG 180
Db 2499 GGGGACATTCGCGGTTTATATAGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTAG 2440

Qy 181 GATTAGTCGGGGGCAAAAGTCATCGGTATATTAATCCATCAACTAAGAATGTCACGA 240
Db 2439 GATTAGTCGGGGGCAAAAGTCATCGGTATATTAATCCATCAACTAAGAATGTCACGA 2380

Qy 241 AATCTAAGTTGTTGAACCTGCTCCGAGCGGTACTCGGTAGGCTGTTTGGCGGTTTACCCC 300
Db 2379 AATCTAAGTTGTTGAACCTGCTCCGAGCGGTACTCGGTAGGCTGTTTGGCGGTTTACCCC 2320

Qy 301 ACCGGTGCATGCGAGACACCAACCAATCAGCAGTCATGCAAGAACCTCTACCAAGCAC 360
Db 2319 ACCGGTGCATGCGAGACACCAACCAATCAGCAGTCATGCAAGAACCTCTACCAAGCAC 2260

Qy 361 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTCCCTAGGCGCAT 420
Db 2259 CATCGAAGTTACATCCAGTACGACCCCATATAGTGCATCGTAGTCCCTAGGCGCAT 2200

Qy 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGGCCACCGCTATCGGGGTGCGATGCTG 480
Db 2199 TGATCACCCAGTTTGGCTCGATCGAGACGTGGCCACCGCTATCGGGGTGCGATGCTG 2140

Qy 481 CCCAGACGGTGTATGGACAGTGTGGTACCTCGATGAGTGGCGAGCATAGTGAAGTCA 540
Db 2139 CCCAGACGGTGTATGGACAGTGTGGTACCTCGATGAGTGGCGAGCATAGTGAAGTCA 2080

Qy 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAAATTT 600
Db 2079 CCAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGCAATTT 2020

Qy 601 ATATGCGCAAAATATTTTGGTACT-----TTATATATAGGAT 641
Db 2019 TTTTAAACAGTTGGGTGTTGGATATAGTGAACAAATGTTTATGTTTATATAGGGA 1960

Qy 642 ATGGCGCTTTTGGCACTATGATTAATTAATCGTATTAATAACAAATATCATCTTTGACT 701
Db 1959 ATGGCGCTTTTGGCACTATGATTAATTAATCGTATTAATAACAAATATCATCTTTGACT 1905

Qy 702 AATTATAAACAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 760
Db 1904 A--ATAACGGATATATCTCAAGGATGCTTTGGCAAGATGAGCGGCGCTTAAACAT 1848

Qy 761 AAGAGCGCTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 820
Db 1847 AAGAGCGCTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800

Qy 821 TTTGGTGATAACTTGGACATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAA 880
Db 1799 TTTGGTGATAACTTGGACATATAAATCTGTATCGTGACGGAACCTTTCTTAAACCTAAA 1740

Qy 881 TATTAAAGACGAGTATTTAAATTTTTCGTGGCAAGTTTCTTGCATCTTATCTAT 940
Db 1739 AGTCAATTTCTGCTTTCTTTTATCTATACCATTTTAAATTCGCAAGAAATGACAGAT 1680

Qy 941 GCCCATTTTACATTTTATCTGTTCTAGCTTCTAGGCTTCTAGGCTTCTAGGCTTCTAGGCT 1000
Db 1679 AGCCACTTTTGGCAGATAGCATCAATTTTAAAGCTATTCAATATTATTAGTTTAAATG 1620

Qy 1001 AAAAATGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1034

Db 1619 AAATAAABAACTCAAAACAAATATATTTTCGTCAAAA 1586

RESULT 2
US-07-828-798C-4/c
; Sequence 4, Application US/07828798C
; Patent No. 5389609
; GENERAL INFORMATION:
; APPLICANT: Holoshuk, Charles P.
; APPLICANT: Meichers, Leo S.
; APPLICANT: Corneliussen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828, 798C
; FILING DATE: 06-APR-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
US-07-828-798C-4

Query Match 29.1%; Score 450.4; DB 1; Length 883;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 ATCTTTGTTTGAATAAATGGAAGAAAGCGTAGGACCATGACCTGGGTGCAACAAT 60
Db 602 ATCTTTGTTTGAATAAATGGAAGAAAGCGTAGGACCATGACCTGGGTGCAACAAT 543

Qy 61 ATTGTTGCTCCTCAAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
Db 542 ATTGTTGCTCCTCAAAATGCTGCAAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 483

Qy 121 TAGGACATTCACCAATTTATATTTGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTTG 180
Db 482 GGGGACATTCGCGGTTTATATAGCGGTGCAATGAAATGCGTGGCAATTCCTCCCACTAG 423

Qy 181 GATTAGTCGGGGGCAAAAGTCATCGGTATATTAATCCATCAACTAAGAATGTCACGA 240

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORGANISM: Nicotiana tabacum
; US-08-315-868A-4

Query Match      29.1%; Score 450.4; DB 2; Length 883;
Best Local Similarity 85.4%; Pred. No. 28-100; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 86;

QY 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGCTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
Db 602 ATCTTTGTTTGAAGAAATTTGGAAGAAATGTTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
QY 61 ATCTTTGTTTGAAGAAATTTGGAAGAAAGCTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
Db 542 ATCTTTGTTTGAAGAAATTTGGAAGAAATGTTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
QY 121 TAGGACATTCACCATTTATATTTGCGGTGCAATGATTCGCGGTGCAATTTCCCTCCACTTG 180
Db 482 GGGACATTCGCGGTTTATATTTAGCGGTACATGATTCGCGGTGCAATTTCCCTCCACTTG 180
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAATCAAT 240
Db 422 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAATCAAT 240
QY 241 AATCTAAGTTGTTGAATCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 300
Db 362 AATCTAAGTTGTTGAATCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 300
QY 301 ACCGGTGCATCTGAGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 302 ACCGGTGCATCTGAGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
QY 361 CATCGAAGTTACATCCAGTACGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
Db 242 CATCGAAGTTACATCCAGTACGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
QY 421 CAATGACCCACGTTTGGCTTCGATCGAGACGTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 480
Db 182 TGATCACCACCAAGTTTGGCTTCGATCGAGACGTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 480
QY 481 CCCAGACGGTGTATGACAGTTGTTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 540
Db 122 CCCAGACGGTGTATGACAGTTGTTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 540
QY 541 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 588
Db 62 CCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 588

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RESULT 3
US-08-315-868A-4/c
; Sequence 4, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828,798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089
; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8622-6
; TELEPHONE/COMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 883
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORGANISM: Nicotiana tabacum
; US-08-315-868A-4

Query Match      29.1%; Score 450.4; DB 2; Length 883;
Best Local Similarity 85.4%; Pred. No. 28-100; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 86;

QY 1 ATCTTTGTTTGAAGAAATTTGGAAGAAAGCTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
Db 602 ATCTTTGTTTGAAGAAATTTGGAAGAAATGTTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
QY 61 ATCTTTGTTTGAAGAAATTTGGAAGAAAGCTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
Db 542 ATCTTTGTTTGAAGAAATTTGGAAGAAATGTTAGGACCAATGACATCTCGGGTACTTTAAGCTGAC 120
QY 121 TAGGACATTCACCATTTATATTTGCGGTGCAATGATTCGCGGTGCAATTTCCCTCCACTTG 180
Db 482 GGGACATTCGCGGTTTATATTTAGCGGTACATGATTCGCGGTGCAATTTCCCTCCACTTG 180
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAATCAAT 240
Db 422 GATTAGTCGGGGGAAAGTCAATCGGTATATTAATTCATCAATCAATCAATCAATCAATCAATCAAT 240
QY 241 AATCTAAGTTGTTGAATCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 300
Db 362 AATCTAAGTTGTTGAATCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 300
QY 301 ACCGGTGCATCTGAGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
Db 302 ACCGGTGCATCTGAGGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
QY 361 CATCGAAGTTACATCCAGTACGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
Db 242 CATCGAAGTTACATCCAGTACGACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
QY 421 CAATGACCCACGTTTGGCTTCGATCGAGACGTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 480
Db 182 TGATCACCACCAAGTTTGGCTTCGATCGAGACGTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 480
QY 481 CCCAGACGGTGTATGACAGTTGTTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 540
Db 122 CCCAGACGGTGTATGACAGTTGTTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 540
QY 541 CAAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 588
Db 62 CCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 588

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RESULT 4
US-08-495-819B-4/c
; Sequence 4, Application US/08495819B
; Patent No. 6037161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Van Den Elzen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
; TITLE OF INVENTION: with Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ladas & Parry
; STREET: 26 West 61st Street

```



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QY 61 ATTGTTCTCTCCAAATGTGGTACAAGATTTGTATCATCTCCGGGTACCTTTAAGCTGAC 120
D 542 ATTGTTCTCTCCAAATGTAGTACAAGGTTATTACATCTCCGGGAACCTTAAGTTCGC 483
QY 121 TAGGACATTCACCAATTTATTTCCCTGCAATTTGGTGGCATTTCCCTCCACTTG 180
D 482 GGGGACATTTGCCCTTTATTTAGCCGTACATGAATTTGATGATTTCCCTCCACTAG 423
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTAAAGAAATGTCCAGA 240
D 422 GGTAGTCGGGGGAAAGTCAATCGGAATTTGAATCCATCAACTAAAGAAATGTCCAGA 363
QY 241 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGCTAGGGTGTGGGGTTTACCCC 300
D 362 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGCTAGGGTGTGGGGTTTACCCC 303
QY 301 ACCGGTGCATTCGAGGACACCAACATCACAGTCAATCGGCTAGGGTGTGGGGTTTACCCC 360
D 302 ACCGGTGCATTCGAGGACACCAACATCACAGTCAATCGGCTAGGGTGTGGGGTTTACCCC 243
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 420
D 242 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 183
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGCGCCACCGCTATCGGGGTGATGCTG 480
D 182 TGATCACCAGTTTGGCTCGATCGAGACGTGCGCCACCGCTATCGGGGTGATGCTG 123
QY 481 CCCAGACGGTGTATGGAAGTGTGCTACCTCGATAGTGGCAGCATTAAGTGAAGTCA 540
D 122 CCCAAAGCGTGTACGGACAGTTGTTCCGACCTCGATAGTGGCAGCATTAAGTGAAGTCA 63
QY 541 CAAAGCAGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGT 588
D 62 CCAAGGCAAGAGGAGGAGAAACAAAGAAAGATCTCAAGTTGCCCATGT 15

RESULT 6
US-08-315-868A-5/C
; Sequence 5, Application US/08315868A
; Patent No. 5856151
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.
; APPLICANT: Meulenhoff, Elisabeth J. S.
; APPLICANT: Sela-Buiriage, Marianne B.
; APPLICANT: Van Den Eizen, Petrus J. M.
; TITLE OF INVENTION: Antifungal Preparations, Process for
; TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants with
; TITLE OF INVENTION: Decreased Susceptibility to Fungi
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315, 868A
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/828, 798
; FILING DATE: 06-APR-1992
; APPLICATION NUMBER: PCT/NL91/00089

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; FILING DATE: 31-05-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mass, Clifford J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-8623-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884
; TYPE: Nucleotide
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; US-08-315-868A-5

Query Match 29.1%; Score 450.4; DB 2; Length 884;
Best Local Similarity 85.4%; Pred. No. 2e-100;
Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 ATCTTTGTTTGAATAAATTTGAAAAAAGCTAGGACCAATGGACCTTGGGTGCAACAT 60
D 602 ATCTTTGTTTGAATAAATTTGAAAAAATGTAGGACCAATGGACCTTGGGTGCAACAT 543
QY 61 ATGTGTCTCTCCAAATGTGGTACAAAGATTTGTATCATCTCCGGGTACTTTAAGCTGAC 120
D 542 ATGTGTCTCTCCAAATGTGGTACAAAGATTTGTATCATCTCCGGGTACTTTAAGCTGAC 483
QY 121 TAGGACATTCACCAATTTATTTCCCTGCAATTTGGTGGCATTTCCCTCCACTTG 180
D 482 GGGGACATTTGCCCTTTATTTAGCCGTACATGAATTTGATGATTTCCCTCCACTAG 423
QY 181 GATTAGTCGGGGGAAAGTCAATCGGTATTTAAATCCATCAACTAAAGAAATGTCCAGA 240
D 422 GGTAGTCGGGGGAAAGTCAATCGGAATTTGAATCCATCAACTAAAGAAATGTCCAGA 363
QY 241 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGCTAGGGTGTGGGGTTTACCCC 300
D 362 AATCTAGTTGTTGAACTGTCGAGGCTACTCGGCTAGGGTGTGGGGTTTACCCC 303
QY 301 ACCGGTGCATTCGAGGACACCAACATCACAGTCAATCGGCTAGGGTGTGGGGTTTACCCC 360
D 302 ACCGGTGCATTCGAGGACACCAACATCACAGTCAATCGGCTAGGGTGTGGGGTTTACCCC 243
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 420
D 242 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTGGCCCTAGGCGCAT 183
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTGCGCCACCGCTATCGGGGTGATGCTG 480
D 182 TGATCACCAGTTTGGCTCGATCGAGACGTGCGCCACCGCTATCGGGGTGATGCTG 123
QY 481 CCCAGACGGTGTATGGAAGTGTGCTACCTCGATAGTGGCAGCATTAAGTGAAGTCA 540
D 122 CCCAAAGCGTGTACGGACAGTTGTTCCGACCTCGATAGTGGCAGCATTAAGTGAAGTCA 63
QY 541 CAAAGCAGAGGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGCCCATGT 588
D 62 CCAAGGCAAGAGGAGGAGGAGAAACAAAGAAAGATCTCAAGTTGCCCATGT 15

RESULT 7
US-08-495-819B-5/C
; Sequence 5, Application US/08495819B
; Patent No. 6087161
; GENERAL INFORMATION:
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Cornelissen, Bernardus J. C.

```

APPLICANT: Meulenhoff, Elisabeth J. S.
 APPLICANT: Sela-Buurlage, Marianne B.
 APPLICANT: Van Den Elzen, Petrus J. M.
 TITLE OF INVENTION: Antifungal Preparations, Process for
 TITLE OF INVENTION: Making Such Preparations, Process for Obtaining Plants
 TITLE OF INVENTION: With Decreased Susceptibility to Fungi
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ladas & Parry
 STREET: 26 West 61st Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10023
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
 COMPUTER: IBM PC/XT/AT or compatibles
 OPERATING SYSTEM: DOS
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/495,819B
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/315,868
 FILING DATE: 30-SEPT-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/828,798
 FILING DATE: 06-APRIL-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/NL91/00089
 FILING DATE: 31-05-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Mass, Clifford J.
 REGISTRATION NUMBER: 30086
 REFERENCE/DOCKET NUMBER: U-010255-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 708-1800
 TELEFAX: (212) 246-8959
 TELEX: 233288
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 884
 TYPE: Nucleotide
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Nicotiana tabacum
 US-08-495-819B-5

Query Match 29.1%; Score 450.4; DB 3; Length 884;
 Best Local Similarity 85.4%; Pred. No. 2e-100;
 Matches 502; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 ATCTTTGTTGAAAAAATTCGAAAGAACGTAGGACCAATGACCTCGGTGCAACAAT 60
 DB 602 ATCTTTGTTGAAAAAATTTGAGAAAATGTAGGACCAACAGTCTTGTGTGCAACAT 543

QY 61 ATTGTTGTCCTCAAAATGCGTCAAGGATGTTATCATCTCCGGGTACTTTAAGCTGAC 120
 DB 542 ATTGTTGTCCTCGGAATAGTACAAGGGTTATTACATCTCCGGGAACCTCAAGTTCCG 483

QY 121 TAGGACATTCACCATTTATATTTGCGGTGATTAATTTGCGTGGCATTTCCCTCCACTTG 180
 DB 482 GGGGACATTCGCGTTTATATTAGCGTACATGAATTCATGCGCATTTCCCTCCACTAG 423

QY 181 GATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAATAAGAAATGTCCAGA 240
 DB 422 GGTAGTCGGGGCGAAAGTCATCGGAATGTTGAATCCATCAATAAGAAATGTCCAGA 363

QY 241 AATCTAAGTTGTTGAATCGTCCGAGCGGTACTCGGCTAGGGTGTGTTGGGGTTTACCCC 300

Db 362 AATCTAACCACCTGAATTTGGTCCAAAGCGTATTTCAGCCAAAGGTGTTTGGTGGTTTACCCC 303
 QY 301 ACCCGGTGCACTGACGACACCCACCAATCACCAGTATCGCAGAACCTTCTACCGCAC 360
 Db 302 ACCCGGTGCACTGACGACACTCCACCAAGTACCGGTTTGGCAGTACCCCTTACCGACG 243
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCTAGTCCCTTACGGCGCAT 420
 Db 242 CATTGAAGTTACAATTTAGTACGGCCCCCATACAGTGCCATTTTGTAGTACCTCGTGGCGCAT 183
 QY 421 CAATGACCCACGTTTGGCTTCGATCGAGAGCGTGGCCACCGCTATCGGGGTGCAATCTG 480
 Db 182 TGATCACCCCAAGTTTGGCTTCGATCGAGAGCGCGGCCACCGCTATCGGGGTGCAATCTG 123
 QY 481 CCCAGACGTTGATGAGCAGTTTGTGGTACCTCGATAGTGGCAGCATAAAGTGAAGTCA 540
 Db 122 CCCAAACGGTGTACGACAGTTGTTTCGGACCTCGATAGTGGCAGCATAAAGTGAAGTCA 63
 QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAAAGATCTCAAGTAGGCCCATGT 588
 Db 62 CCAAGGCAAGGAGGAGGAGAAACAAAGAAAGATCTCAAGTTGCCCATGT 15

RESULT 8
 US-09-589-733C-4/c
 ; Sequence 4, Application US/09589733C
 ; Patent No. 6677503
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duwick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 875
 ; TYPE: DNA
 ; ORGANISM: Helianthus annuus
 US-09-589-733C-4

Query Match 11.7%; Score 180.6; DB 4; Length 875;
 Best Local Similarity 60.9%; Pred. No. 1e-34;
 Matches 332; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 1 ATCTTTGTTGAAAAAATTCGAAAGAACGTAGGACCAATGACCTTGGGTGCAACAAT 60
 DB 577 ATCTGGTCTTGAAAAACCTTGATAATCAGTTGGTCCCAATTTCCAGAGTTGCAACAAT 518

QY 61 ATTGTTGTCCTCAAAATGCGTACAGGATGTTATCATCTCCGGGTACTTTAAGCTGAC 120
 DB 517 ACTGATCAGTTTGTACACCGTGCAGGGTTATTGACCCCGCAGGAGCCCGTAACCTAC 458

QY 121 TAGGACATTCACCATTTATATTTGCGGTGATTAATTTGCGTGGCATTTCCCTCCACTTG 180
 DB 457 CAGGACATTCGCTTATTCATCCGACGTACATGAGATACCCCGGTGCACCC-----AT 404

QY 181 GATTAGTCGGGGCGAAAGTCATCGGTATATTAATCCATCAATAAGAAATGTCCAGA 240
 DB 403 TAGAATTTGGTCTAAACACCATCGGCATTTGAATCCGTCACAAAGAAATGTCAAGA 344

QY 241 AATCTAAGTTGTTGAATCGTCCGAGCGGTACTCGGCTAGGGTGTGTTGGGGTTTACCCC 300
 DB 343 AATCAAGTTGTTGAATCGTCCGAGCGGTACTCGGCAATGTGTTGGGTGGGTACCAT 284

QY 301 ACCGGTCACTGAGGACACACCAATCACCAGTCATGACGAACTTACCAGCAC 360
Db AGTTTGGCANTGGAGGAGACCGTTGCAATCACCGGCTGACACTGCTCGCCGCAAC 224
QY 361 CATGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTGCCCTCGGCGCAT 420
Db CATCAAGTTGCAATTGGTTCCGGGCCATATACGGGCTCCTGCTGTCAGCTCGGACGG 164
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTCGGCCACCGCTATCGGGTGCATGCTG 480
Db TTAAGACCGAGTTTGGCTGAGTTAAGTTGTCGGCGCCACC---AGGCACCCGACAG 107
QY 481 CCCAGCGGTGTATGACGAGTTTGGCTGCTCATATAGTGGCAGCATAAAGTCA 540
Db CCCAACCGTGTATGACAGTTTTCGAATAGTGAACCGGCTGCAATTGATATAGTAA 47
QY 541 CAJAA 545
Db 46 AAAGA 42

RESULT 9
US-08-181-271A-4/c
; Sequence 4, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-181-271A-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTTGAAGAAATGGAAGACGCTAGGACCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCCTTAAAGAAATCTCGACAATCAGTAGGCCACATGATCCAGGCCCATTTGTAT 545
QY 55 AACATATTTGTTGCTCTCCAAATGTTGGAACAAGATTGTTACATCTCCGGGTACTTTAA 114
Db 544 AACAAATATTCAATTGGTTTTTATCAGAGTACATGTTGTTACATCCACCTTGTGTTTTCA 485
QY 115 GCTGACTAGGACATTCACCATTTATATTTGCGTGCATTGAATTGCGTGGCAATTTCCCTC 174
Db 484 ACTGTGCTGGGCAATTTGCTTTAATAGTGTGCTGTCATCTGAGATTACACATCTCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGCGGAAAGTCATCGGTATATTAAATCCATCAACTAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAGAGAGATGT 374
QY 235 CCCAGAAATCTAAGTTGTTGAACTGGTCCGAGCGCTACTCCGCTAGGTTGTTGGGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTCAAAATTCAGCTAAAGTTTAGGTGCTT 317
QY 295 TACCCCAACCCCGTGCATCTGACGAGACACCAACCAATCACCAGTCATGACGAACTCTAC 354


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316 TTCCATAGCCTTGACATCTTACATCCGTTACAGTCTCAGTCTCACAATACCTCGGC 257
355 CAGCACCATCGAAGTTACATCCAGTAGCAGCCCATATACGTGCGATCGTAGTCCCTTAG 414
256 CACTGCCATCGAAGTTGCAATGGTTCCAGCCCAATGCGAGCTGGACTGTTCTCTGGGT 197
415 GCGCATCAATGACCCAGCTTTGGCTCGATCGAGAGCTGCGCCACCGCTATCGGGGTG 474
196 TCACATTAATGCTCAAGATGGCTGAGTCGAGCCGCTGCTCACCT---GGAGAGG 140
475 ATGCTGCCAGAGCGGTGTATGACAGTGTGTGGTACCTCGATAGTGGCAGCATAAGTGA 534
139 CCGCGGCCAGACTGTGTAGTGCATTGTTGACAATGTCAAAAGTGGCAGCATGAGTAA 80
535 AAGTCACAAA 544
79 CAGCTACAAA 70

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RESULT 10

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US-08-449-315-4/c
; Sequence 4, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-449-315-4
; Query Match 10.3%; Score 159.2; DB 1; Length 900;
; Best Local Similarity 61.1%; Pred. No. 1.7e-29;
; Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTGAAAAAATGGAAAAAGAACGTAGAACACATF-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCCACCATGATCCAGGCCCAATTTGTAC 545
QY 55 AACAAATATTGTTGCTCCCAATGTTGTAAGGATTGTTACATCTCCCGGTACTTTAA 114
Db 544 AACAAATATTGTTGTTTATTCACAGTACATGTTGTTTACATCCACCTTGTGTTTCA 485
QY 115 GCTGACTAGGACATTCACCAATTTATTTTCGCGTGCATTTGAATTCGTTGGCATTCCTC 174
Db 484 ACTGTGCTGGGCAATTTGTTGTTAATAGTGTGTCATCTGAGATTACGACATCCTCC-- 427
QY 175 CACTTGGATTAGTCGGGCGGAAGTTCATCGTATATTAAATCCATCACTAAAGAAATGT 234
Db 426 -----ATTGGTCGGGCTGAAATTCCTATGGGATGTTAAATCCATCAAGAGAGATGT 374
QY 235 CCCAGAAATCTAAGTGTGTTGAACCTGGTCCGAGGCGGTACTCGGCTAGGTTGTTGGCGGTT 294
Db 373 CGACAAAGTCT---CTGATTGGGTTGTTAATAGTGCAAAATTCAGCTAAAAGTGTAGGTGTT 317
QY 295 TACCCACCCCGGTGCTGACCTGAGGACACCAACCAATCACCATGTCATGACGAACTCTAC 354

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Db 316 TTCCATAGCCCTTGACACTCTAACCTCCGGTTACAGTCTCAGTCTCAAAATTACCTCGGC 257
Qy 355 CAGCACCATCAAGTTACATCAGTACGACCCCATATACGTGCCATCGTAGTGCCTTAG 414
Db 256 CACTGCCATCAAGTTGCAATTTGGTTGATCGACCCCAATGCGAGCTTGGACTGTTCTCGGT 197
Qy 415 GCGCATCAATGACCCAGCTTTGGCTCGATCGAGAGCTCGGCCACCGCCTATCGGGTGC 474
Db 196 TCACATTAATGCTCCAAGATTGGCTGAGTGCAGCCGCTGCTCCACCT---GGAGAGG 140
Qy 475 ATGTGCCAGCAGCGTGTATGACAGTGTGTGCGTACCTCGATAGTGGCAGCATAAGTGA 534
Db 139 CCGCGGCCAGACTGTGTAGTGTGATTTGTGACAATGTCAAAAGTGGCAGCATGAGTAA 80
Qy 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 11

US-08-444-803-4/c
Sequence 4, Application US/08444803
Patent No. 5654414

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444.803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-444-803-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;

Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

Qy 1 ATCTTTGTTTGAATAAATTGAAAGAACGTAGGACCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAATAATCTCGACAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
Qy 55 AACAAATATTGTTGCTCTCCAAATGTGGTACAGGATGTGTACATCTCCGGGTACTTTAA 114
Db 544 AACAAATATTGTTGTTTATACAGTACATGTTGTATACATCCACCTTGTGTTTCA 485
Qy 115 GCTGACTAGGACATTCACCATTTATATTGCGGTGCAATGCGTGGCATTTCCCTC 174
Db 484 ACTGTGCTGGGCATTTGTTGTTAATAGGTGCTGTGCACTGAGATTACACATCTCTCC-- 427
Qy 175 CACTTGGATTAGTCGGGGCGAAAGTCAATCGGTATATTAAATCCATCAACTAAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATCGGGATGTTAAATCCATCAACAGAGAGATGT 374
Qy 235 CCAGAAATCTAAGTTGTTGAATGCTCGAGCGGTACTCGGTAGGGTGTGTTGGCGGT 294
Db 373 CGACAAAGTCT---CTGATTGGGTGTTAAGTGCATAAATCAGTAAAGTGTGTAGGTGCTT 317
Qy 295 TACCCTCCCGCGGTGCACTGCGAGGACACACCAATCACCAGTCATGTCACGAACTCTAC 354

Db 316 TTCCATAGCTTGACACTCTAACATCCCGTTTACAGTCTCCAGTCTCACAATACCTCGGC 257
QY 355 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTAG 414
Db 256 CACTGCCATCGAAGTTGCAATGTTGACCCCAATGCGAGCCTGGAAGTCTTCTGGGT 197
QY 415 GCGCATCAATGACCCAGCTTTGGCTCGATCGAGACGTGCGCCACCCCTATCGGGTGC 474
Db 196 TCATTAAATGCTCAAGATTGGCTGAGTCGAGCCGCTGCCACCT--GGAGAGG 140
QY 475 ATGCTGCCAGACCGTGTATGACAGTGTGCTACTGATAGTGGCAGCATAGTGA 534
Db 139 CCGGGGCCAGACTGTGTAGTGCATTTGTTGCAATGTCAAAAGTGGCAGCATGATGA 80
QY 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 12

US-08-449-043-4/c
; Sequence 4, Application US/08449043
; Patent No. 5689044

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
APPLICATION NUMBER:
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-449-043-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

QY 1 ATCTTTGTTTGAATAATGGAAGAACGTAGACCCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTCTCTTAAATAATCTCGACAAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACAAATATTGTGCTCCAAATGTGTACAAAGATTGTTACATCTCTCCGGGTACTTTAA 114
Db 544 AACAAATATTGTTTATTCACAGTACATGGTGTGTTACATCCACCTTGTGTTTCA 485
QY 115 GCTGACTAGGACATTCACCATTTATTTGCGGTGCGATTGAATTCGCGGCAATTCCTC 174
Db 484 ACTGTGCTGGGCATTTGTTGTTTAAATAGTGTGTCGATCTGAGATTACGACATCCTCC-- 427
QY 175 CACTTGGATTAGTCGGGCGGAAAGTCATCGGTATTTAAATCCATCAACTAAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGNAATTCATGGGATGTTAAATCCATCAACAGAGATGT 374
QY 235 CCCAGAAATCTAAGTGTGTTGAACGTGGTCCGAGGCGTACTCGGCTAGGGTGTGTTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAATTCAGCTAAAGTGTAGTGCTT 317
QY 295 TACCCACCCCGGTGCTACTGCGAGGACACCACCAATCACCAGTCATGCGAAGACCTCTAC 354

Db 316 TTCCATAGCCTTGACACTCTAACCTCCGTTACAGTCTCCAGTCTCAAAATTACCTCGGC 257
QY 355 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTGGCCCTAG 414
Db 256 CACTGCCCATGAAGTTGAATGTTGACCCCAATGCGAGCCTGGAAGTGTCTCTGGGT 197
QY 415 GCGCATCAATGACCCACGCTTTGGCTCGATCGAGACGTCGGCCACCGCCTATCGGGTCG 474
Db 196 TCACATTAATGCTCCAAGATTGGCTGAGTCGAGCGCCTGCTCCACCT---GGAGAG 140
QY 475 ATGCTGCCACGAGCTGTATGGAAGTTGTCGTACTCGATAGTGGCAGCATAAAGTGA 534
Db 139 CCGGGGCCAGACTGTGTAGTGCATTGTTGACAATGTCAAAAGTGGCAGCATGAGTAA 80
QY 535 AAGTCACAAA 544
Db 79 CAGTACAAA 70

RESULT 13
US-08-456-265A-4/c
; Sequence 4, Application US/08456265A
; Patent No. 5767369
; GENERAL INFORMATION:
; APPLICANT: Alexander, Danny C.
; APPLICANT: Ryals, John A.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Stinson, Jeffrey R.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,265A
; FILING DATE: 31-MAY-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
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FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-456-265A-4
Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTGAAAAAATTGAAAAGACGTAGGACCACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCGCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACAATATTGTTCTCTCCAAATGTGTTACAGGATTGTATACATCTCCGGGTACTTTAA 114
Db 544 AACAATATTGTTCTCTCCAAATGTGTTACAGGATTGTATACATCTCCGGGTACTTTAA 485
QY 115 GCTGACTAGGACATTCCACATTTATATTTGCCGTGCATTGAATTCGTCGGCATTTCCCTC 174
Db 484 ACTGCTCTGGCATTTGTTGTTAATAGTGTCTGTGCATCTGAGATTACGACATCTCTCC 427
QY 175 CACTTGGATTAGTCGGGGGAAAGTCATCGGTATATTAATCCATCAACTAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATGGGGATGTTAAATCCATCAACAAGAGATGT 374
QY 235 CCAGAAATCTAAGTTGTTGAACTGCTCGAGCGTACTCGGTAGGGTGTGTTGGGGTT 294
Db 373 CGAAGAAGTC---CTGATTGGGTGTTAATAGTGCATAATTCAGCTAAGTGTAGGTGCTT 317
QY 295 TACCCCAACCGGTGCACTCGAGGACACCAACAATCAACAGTCATGCGACGAACTCTAC 354
Db 316 TTCCATAGCCTTGACACTCTAAACATCCCGTTACAGTCTCCAGTCTCACAATTAACCTCGC 257
QY 355 CAGCACCATCGAAGTTACATCCAGTACGACCCCATATAGTCATCTAGTGCCTTAG 414
Db 256 CACTGCCATCGAAGTTGCAATGTTGTTGACCCCAATGCGAGCCTGGACTGTTCTGGGT 197
QY 415 GCGCATCAATGACCCACGTTTGGCCTTCGATCGAGAGCGTCGGCCACCGCCTATCGGGGTG 474
Db 196 TCACATTAATGCTCCAAAGATTGSCCTGAGTCGAGCGCCCTGCTCCACCT---GGAGAG 140
QY 475 ATGCTGCCACGAGCGGTGTATGGACAGTTGTTGGCTACTCGATGTCGAGCAGTAAAGTGA 534

Db 139 CCGGGCCCACTGTGTAGTGCATTTGTTGACAAATGTCAAAGTGGCAGCATGAGTAA 80

QY 535 AAGTCACAAA 544

Db 79 CAGCTACAAA 70

RESULT 14

US-08-455-416-4/c

; Sequence 4, Application US/08455416

; Patent No. 577200

GENERAL INFORMATION:

; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,416
; FILING DATE: 31-MAY-1995

CLASSIFICATION:

; CLASSIFICATION: 800

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/181,271

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-455-416-4

Query Match

Best Local Similarity 10.3%; Score 159.2; DB 1; Length 900;

Mismatches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;

QY 1 ATCTTTGTTTCAAAAAATTTGAAAAAGACGTAGGACACACAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTTAAAAATCTCGAATAATCAGTAGGCCACATGATCCAGGCCCATTTGTAC 545
QY 55 AACAAATATTGTTGCTCTCCAAATGTGGTACAAAGATTGTTTACATCTCTCCGGGTACTTTAA 114
Db 544 AACAAATATTGTTGCTCTCTCCAAATGTGGTACAAAGATTGTTTACATCTCTCCGGGTACTTTAA 485
QY 115 GCTGACTAGGACATTCACCATTTATTTGCGGTGCAATTGAATTCGCTGGCATTTCCTC 174
Db 484 ACTGTGCTGGGCATTTGCTGTTAATAGTGTCTGTCATCTGAGATTACGACATCTCTCC-- 427
QY 175 CACTTGGATTAGTCGGGCGGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGT 234
Db 426 -----ATTGCTGGGCTGAATTCATGGGATGTTAAATCCATCAACAAGAGAGATGT 374
QY 235 CCGAGAAATCTAAGTTGTTGAACTGGTCCGAGGGGTACTCGGCTAGGGTGTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTGGGTTGATTAAAGTGCAAAATTCAGCTTAAAGTTGTTAGTGCTTT 317
QY 295 TACCCACCCCGGTGCATCTGCAGGACACACACCAATCACAGTCATCGACGAACCTCTAC 354
Db 316 TTCCATAGCCTTGACACTCTAACATCCGGTTACAGTCTCCAGTCTCACATTAACCTCGGC 257
QY 355 CAGCACCATCGAAGTTACATCCAGTACACCCCATATACGTGCCATCGTAGTGGCCCTAG 414
Db 256 CACTGCCATCGAAGTTGCAATTTGGTTCGACCCCAATGCGAGCGCTGGACTGTTCTGGGT 197
QY 415 CGGCATCAATGACCCCGTTTGGCTCTGATCGAGACCTTCGCGCCACCGCTTATCGGGTGC 474
Db 196 TCACATTAATGCTCAAGATTGGCTGAGTCGAGCCGCTGCTCCACCT---GGAGAGG 140
QY 475 ATGTGCCAGACGGTGTATGACAGATTGTTGGGTACCTCGATAGTGGCAGCATAGTGA 534

Db 139 CCGCGGCCGACGCTGTGTAGTGTGATTTGACAAATGTCAAAAGTGCAGCAATGAGTAA 80
QY 535 AAGTCACAAA 544
Db 79 CAGCTACAAA 70

RESULT 15

US-08-455-244-4/c.
; Sequence 4, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-455-244-4

Query Match 10.3%; Score 159.2; DB 1; Length 900;
Best Local Similarity 61.1%; Pred. No. 1.7e-29;
Matches 336; Conservative 0; Mismatches 193; Indels 21; Gaps 4;
QY 1 ATCTTTGTTTGAATAAATCGAAAGACGCTAGGACCAAT-----GGACCTTGGGTGC 54
Db 604 ATCTTTCTTAAAAAATCTCGACAAATCAGTAGGCGCCACATATCCAGGCCCATTTGTAC 545
QY 55 AACAAATTTGTTGCTCTCCAAATGTTGACAGGATTTTACATCTCCGGGTACTTTAA 114
Db 544 AACAAATTTCAITGGTTTTTATCAGAGTACATGGGTGTTTATCATCCACCTTGTTTCA 485
QY 115 GCTGACTAGGACATTCACCAATTTATATTTGCCGTGCATTTGAATTCGCTGGCATTTCCCTC 174
Db 484 ACTGTCTGGCATTTGTTGTTAATAGGTGCTGTGTCATCTGAGATTACGACATCTCTCC-- 427
QY 175 CACTTGGATTAGTCGGGGGAAAGTCACTCGGTATATTAATTCATCACTAAGAAATGT 234
Db 426 -----ATTGTCGGGCTGAATTCATCGGGATGTTAAATCCATCAACAGAGAGATGT 374
QY 235 CCGAGAAATCTAAGTTGTTGAACTGCTCGAGCGGTACTCGGTAGGTGTTTGGCGGTT 294
Db 373 CGACAAAGTC---CTGATTTGGGTGTTAATGTCGCAATTCAGCTAAGTTAGGTGCTT 317
QY 295 TACCCCAACCGGTGCACTCGAGGACACCAACAAATCACAGTCATGACAGAACCTCTAC 354
Db 316 TTCCATAGGCTTGACACTCTAAACATCCCGTTACAGTCTCAGTCTCACAATTAACCTCGGC 257
QY 355 CAGCACCATCGAGTTTACATCCAGTACGACCCCATATAGTCGTCATCTAGTGCCTTAG 414
Db 256 CACTGCCATCGAAGTTGCAATTCGTTTCGACCCCAATGCGAGCTCGGACTGTTCTGGGT 197
QY 415 GCGCATCAATGACCCACGTTTGGCTTCGATCGAGAGCTCGGCCACCGCTATCGGGGTG 474
Db 196 TCACATTAATGCTCCAGATTTGSCCTGAGTCGAGCGGCTGCTCCACCT---GGAGAGG 140
QY 475 ATGCTGCCACGACGGTGTATGGACAGTTGTTGCGTACCTCGATGCTAGTGGCAGCATAGTGA 534

Db	139	CCGCGGCCCGAGCTGTGTAGTGCATTTGTTGACAAATGTCAAAAGTGGCAGCATGAGTAA	80
Qy	535	AAATCACAAA	544
Db	79	CAGCTACAAA	70

Search completed: August 18, 2004, 16:17:40
 Job time : 122.074 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 03:35:10 ; Search time 5856.14 Seconds
(without alignments)
11442.406 Million cell updates/sec

Title: US-10-051-307-3
Perfect score: 1546
Sequence: 1 atctttttgaaaaaatg.....tggtgaagttggtgtttc 1546

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb.htg.*
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22: em.ov.*
23: em.pat.*
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25: em.pl.*
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33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rtd.*
36: em.htg.nam.*
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38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	1334.4	86.3	1598	6	AX665979	AX665979 Sequence
C 4	715	46.2	2659	8	SC81OLP	X72927 S.commerson
C 5	563.6	36.5	2638	8	SC13OLP	X72928 S.commerson
C 6	550.4	35.6	1304	8	AF093743	AF093743 Lycopersi
C 7	508	32.9	901	8	SC08MLP	X67121 S.commerson
C 8	500	32.3	2033	8	NT08PR	X95308 N.tabacum o
C 9	500	32.3	3033	6	AR037158	AR037158 Sequence
C 10	499.4	32.3	3033	6	S40046	S40046 abscisic ac
C 11	485.2	31.4	977	8	NTAP24G	X65701 N.tabacum a
C 12	483.4	31.3	917	8	SCA81OLP	X72926 S.commerson
C 13	480.4	31.1	729	8	AY093595	AY093595 Lycopersi
C 14	480.4	31.0	744	8	AF473702	AF473702 Solanum n
C 15	467.6	30.2	818	8	AF450276	AF450276 Solanum n
C 16	467.6	30.2	937	8	AY007309	AY007309 Solanum d
C 17	465.4	30.1	856	8	AF297646	AF297646 Capsicum
C 18	458.6	29.7	832	8	CAN297410	AJ297410 Capsicu
C 19	458.6	29.7	832	6	LET0M1M	X66416 L.esculentu
C 20	450.4	29.1	883	6	A16780	A16780 osmotin-lik
C 21	450.4	29.1	883	6	AR027097	AR027097 Sequence
C 22	450.4	29.1	883	6	AR103205	AR103205 Sequence
C 23	450.4	29.1	884	6	A16782	A16782 osmotin-lik
C 24	450.4	29.1	884	6	AR027098	AR027098 Sequence
C 25	450.4	29.1	884	6	AR103206	AR103206 Sequence
C 26	450.4	29.1	961	8	NTAP24	X65700 N.tabacum m
C 27	449.4	29.1	845	8	LEP0PA	X70787 L.esculentu
C 28	448.4	29.0	741	6	A83550	A83550 Sequence 1
C 29	448.4	29.0	741	6	BD082734	BD082734 Antifunga
C 30	444.6	28.8	928	8	S44889	S44889 osmotin-pat
C 31	443	28.7	917	8	TOMNP24	M21346 Tomato NP24
C 32	431	27.9	971	8	AF376058	AF376058 Petunia x
C 33	422.4	27.3	738	8	NTOSMOTIN	X61679 N.tabacum m
C 34	421.6	27.3	541	8	AY256440	AY256440 Solanum t
C 35	421.6	27.3	542	8	AY256441	AY256441 Solanum t
C 36	420.2	27.2	526	8	AY256436	AY256436 Solanum t
C 37	420	27.2	593	8	AY256429	AY256429 Solanum t
C 38	419.6	27.1	567	8	AY256439	AY256439 Solanum t
C 39	417.4	27.0	535	8	AY256434	AY256434 Solanum t
C 40	416.6	26.9	538	8	AY256431	AY256431 Solanum t
C 41	415.6	26.9	539	8	AY256430	AY256430 Solanum t
C 42	414	26.8	510	8	AY256425	AY256425 Solanum t
C 43	411	26.6	621	8	AF450277	AF450277 Solanum n
C 44	407.8	26.4	541	8	AY256428	AY256428 Solanum t
C 45	406.6	26.3	542	8	AY256437	AY256437 Solanum t

ALIGNMENTS

RESULT 1
AX665980
LOCUS AX665980 1546 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02059333.
ACCESSION AX665980
VERSION AX665980.1 GI:29290849
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
TITLE Gene promoters isolated from potato and use thereof

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 02059333-A 3 01-AUG-2002;
 Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)
 FEATURES Location/Qualifiers
 source 1..1546
 /organism="Solanum tuberosum"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4113"

ORIGIN

Query Match 99.9%; Score 1545; DB 6; Length 1546;
 Best Local Similarity 100.0%; Pred. No. 4.2e-302; Indels 0; Gaps 0;
 Matches 1546; Conservative 0; Mismatches 0;

QY 1 ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGGACCTGGGTGCAACAAT 60
 DB 1 ATCTTTGTTGAAAAAATGGAAAAAGACGTAGGACCAATGGACCTGGGTGCAACAAT 60
 QY 61 ATTGTTGTCCTCCAAATCGGTACAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
 DB 61 ATTGTTGTCCTCCAAATCGGTACAGGATGTTACATCTCCGGGTACTTTAAGCTGAC 120
 QY 121 TAGGACATTCACCAATTTATATTGCGGTGCAATGAAATGGCGTCAATTCCTCCACTTG 180
 DB 121 TAGGACATTCACCAATTTATATTGCGGTGCAATGAAATGGCGTCAATTCCTCCACTTG 180
 QY 181 GATTAGTCGGGGCGAAGTCACTCGGTATATTTAAATCCATCAATCAATCAATCAATCAAT 240
 DB 181 GATTAGTCGGGGCGAAGTCACTCGGTATATTTAAATCCATCAATCAATCAATCAATCAAT 240
 QY 241 AATCTAAGTCTGTAACCTGGTCCGAGCGGTACTCGGTAGGCTGTTGGCGGTTTACCCC 300
 DB 241 AATCTAAGTCTGTAACCTGGTCCGAGCGGTACTCGGTAGGCTGTTGGCGGTTTACCCC 300
 QY 301 ACCGGTGCATCGAGGACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
 DB 301 ACCGGTGCATCGAGGACACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 360
 QY 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTAGGGCGCAT 420
 DB 361 CATCGAAGTTACATCCAGTACGACCCCATATACGTGCGCATCGTAGTCCCTAGGGCGCAT 420
 QY 421 CAATGACCCAGCTTTGGCCTCGATCGAGAGCGTGGCCACCGCCTATCGGGGTGCGATGCTG 480
 DB 421 CAATGACCCAGCTTTGGCCTCGATCGAGAGCGTGGCCACCGCCTATCGGGGTGCGATGCTG 480
 QY 481 CCCAGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCGAGCATAGTGAAGTCA 540
 DB 481 CCCAGACGGTGTATGGACAGTTGTTGGTACCTCGATAGTGGCGAGCATAGTGAAGTCA 540
 QY 541 CAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 600
 DB 541 CAAAAGCAAGAGGAGGAGAAACAAAAGAGATCTCAAGTAGCCCATGTTTGGTGAATTT 600
 QY 601 ATATGTCGACAAATATTTTGGTACCTTTATATAGGATATAGGATATAGGATATAGGATAT 660
 DB 601 ATATGTCGACAAATATTTTGGTACCTTTATATAGGATATAGGATATAGGATATAGGATAT 660
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 DB 661 TGGATATTAATCGTATTAATCAATATCATATCTTTGACTAATTAATTAATTAATTAAT 720
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 DB 721 TACAATATGATTTGGTAAACGTTGAGGTGCAAAATGTTATAGAGCGCGCTTAATTAATTA 780
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 QY 841 ATAAACTCTGTATCGTGACGAACTTTTCTTAAACTAAATATTAATAAGACGCTATTTT 900
 DB 841 ATAAACTCTGTATCGTGACGAACTTTTCTTAAACTAAATATTAATAAGACGCTATTTT 900

QY 901 AATATTTTTCGTGGCCAAAGTTTCTTGCACTATCTATGATGCCCCATTTTACTTTTATCG 960
 DB 901 AATATTTTTCGTGGCCAAAGTTTCTTGCACTATCTATGATGCCCCATTTTACTTTTATCG 960
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 DB 1021 AGTTTTTTTTCATATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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 DB 1081 ATTCTGATTTTAAAAATCATAACTATTCTGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 AAGTGTGATTTTATCTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 AAGTGTGATTTTATCTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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 DB 1201 AAAAGAACCCCTATTGATGCAAAAGTCAATAAATTAATTAATTAATTAATTAATTT 1260
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 DB 1261 TTACGATCGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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 DB 1321 AGTCATCAAGCTTATCGTGCATCCACATTCCTTCCCTATCTCTATAAATATCTATATACC 1380
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 DB 1381 AAACAGTGGATCATATATAATTTAGTTTCCCTATCTCTATAAATATCTATATACC 1440
 QY 1441 TCTTAACTAAATGATCATCTTAAACACACAAATTAATTAATTAATTAATTAATTAATTTGCA 1500
 DB 1441 TCTTAACTAAATGATCATCTTAAACACACAAATTAATTAATTAATTAATTAATTAATTTGCA 1500
 QY 1501 GAATTAATGAGGCAAAATAGTCTATGTTGAAAGTTGGTCTCTTTC 1546
 DB 1501 GAATTAATGAGGCAAAATAGTCTATGTTGAAAGTTGGTCTCTTTC 1546

RESULT 2
 AX665978 1595 bp DNA linear PAT 26-MAR-2003
 LOCUS Sequence 1 from Patent WO02059333.
 DEFINITION
 AX665978
 ACCESSION
 VERSION AX665978.1 GI:29290847
 KEYWORDS
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE 1
 AUTHORS Dai, Z., Shi, L. and Hooker, B.S.
 TITLE Gene promoters isolated from potato and use thereof
 JOURNAL Patent: WO 02059333-A 1 01-AUG-2002;
 Dai, Ziyu (US); Shi, Lifang (US); Hooker, Brian, S. (US)
 FEATURES Location/Qualifiers
 source 1..1595
 /organism="Solanum tuberosum"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4113"
 ORIGIN
 Query Match 88.1%; Score 1362.4; DB 6; Length 1595;
 Best Local Similarity 94.1%; Pred. No. 3.4e-265;
 Matches 1460; Conservative 0; Mismatches 82; Indels 9; Gaps 4;

QY 1 ATCTTTGTTGAAATTTGAAATGAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 60
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QY 49 ATCTTTGTTGAAATTTGAAATGAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 108
DB |||||
QY 61 ATTGTGTCCTCCAAATGTTGTAACAAGATTTGTTACATCTCTCCGGGTACTTTAAGCTGAC 120
DB |||||
QY 109 ATTGTGTCCTCCAAATGTTGTAACAAGATTTGTTACATCTCTCCGGGTACTTTAAGTTGAC 168
DB |||||
QY 121 TAGGACATTCACCAATTTATTTGCGGTGCAATGAAATGCGTGCATTTCCCTCCACTTG 180
DB |||||
QY 169 CAGGCAATTCACCAATTTATATTTGCGGTGCAATGAAATGCGTGCATTTCCCTCCACTTG 228
DB |||||
QY 181 GATTAGTCGGGGCGAAAGTCATCGGTATATTAATTAATCCATCAACTTAAAGAAATGTCACAGA 240
DB |||||
QY 229 GATTAGTCGGGGCGAAAGTCATCGGTATATTAATTAATCCATCAACTTAAAGAAATGTCACAGA 288
DB |||||
QY 241 AATCTAAGTTGTTGAACTGTCGAGGCGTACTCGGTAGGCTTTGGGGTGTTCACCC 300
DB |||||
QY 289 AATCTAAGTTGTTGAACTGTCGAGGCGTACTCGGTAGGCTTTGGGGTGTTCACCC 348
DB |||||
QY 301 ACCCGGTGCACTGAGGACACACCAATCACCAGTCATGACGAACTCTACACGAC 360
DB |||||
QY 349 ACCCGGTGCACTGAGGACACACCAATCACCAGTCATGACGAACTCTACACGAC 408
DB |||||
QY 361 CATCGAAGTTACATCCAGTACGACCCCATATATGTCATGTCAGTGCAGCACTCTACACGAC 420
DB |||||
QY 409 CATCGAAGTTACATCCAGTACGACCCCATATATGTCATGTCAGTGCAGCACTCTACACGAC 468
DB |||||
QY 421 CAATGACCCAGTTTGGCTCGATCGAGACGTCGCGGACCGCTATCGGGTGCATGCTG 480
DB |||||
QY 469 CAATGACCCAGTTTGGCTCGATCGAGACGTCGCGGACCGCTATCGGGTGCATGCTG 527
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QY 481 CCCGACGCTGTATGGACAGTTGTTGCTGCTACTCGATGTCGACGATAGTGAAGTCA 540
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QY 528 CCCGACGCTGTATGGACAGTTGTTGCTGCTACTCGATGTCGACGATAGTGAAGTCA 587
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QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT 600
DB |||||
QY 588 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAATTT 647
DB |||||
QY 601 ATATGTGACAAATTTATTTTGGTACTTTATATATAGGATATGCGGCTTTTGGCACTA 660
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DB |||||
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DB |||||
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QY 828 TTATTTATGAATATAGACTATAGTTTCAAGTGAACCTTTATTTGGTGATTAATTTGGACAT 887
DB |||||
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QY 888 ATAACTCTGATCTGAGCGAACTTTTCTTAAACTTAATATATAAAGCAGCTATTTT 947
DB |||||
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DB |||||
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QY 961 TTCTAGCCCTTTAGTACCGCTTTGAACATATAAATAATCAATAAATGAAAGTAAAAAT 1020
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DB |||||
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QY 1068 AGTTTATTTTTCATATTAATCTGATGATCATTTGTTAGATCAATGTAATATACAA 1127
DB |||||
QY 1078 ATCATTTCTGATTTTAAATATCAATAATCTGATGATGGAACGCTCTATGCTGATTCGT 1137

DB 1128 ACCATTTCTGATTTTAAATCAACCAATCTCCCAAGGGAAGTCTAT---GTGATCCGT 1184
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DB 1185 GACAAGTGTGTTGATTTTAAATCTGATGAGTCAACAATTTTGTAGTGAATAATCT 1244
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QY |||||
DB 1256 TATTTTACGATCGGAGCATGATACATTTACTAAATTTAAATTTAAATTTGGAAGAAATGAT 1315
DB |||||
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DB |||||
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DB 1376 AGAGAAACCAAGTGGATCATGTATATTTAGTTTCCCTATCTCTCTATATAATATCTATAT 1435
DB |||||
DB 1425 AGAGAAACCAAGTGGATCATGTATATTTAGTTTAAATTTAAATTTATCTATATCTATAT 1484
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DB 1436 ATACCTCTTAAACTTAAATGATCTTAAACACAAATATTAATTTAAATTTTAAAGAA 1495
DB |||||
DB 1485 ATACCTCTTAAACTTAAATGATCTTAAACACAAATATTAATTTAAATTTTAAAGAA 1544
QY |||||
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DB |||||
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RESULT 3
AX665979
LOCUS AX665979 1598 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2 from Patent WO02059333.
ACCESSION AX665979
VERSION AX665979.1 GI:29290848
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
REFERENCE 1 Dai, Z., Shi, L. and Hooker, B.S.
AUTHORS Gene promoters isolated from potato and use thereof
TITLE Patent: WO 02059333-A 2 01-AUG-2002;
JOURNAL Dai, Ziyu (US) ; Shi, Lifang (US) ; Hooker, Brian, S. (US)
FEATURES Location/Qualifiers
source 1. .1598
/organism="Solanum tuberosum"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 86.3%; Score 1334.4; DB 6; Length 1598;
Best Local Similarity 93.8%; Pred. No. 1.6e-259;
Matches 1456; Conservative 0; Mismatches 87; Indels 10; Gaps 6;
QY 1 ATCTTTGTTGAAATTTGAAATGAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 60
DB |||||
QY 49 ATCTTTGTTGAAATTTGAAATGAAAGACGTAGGACCAACATGGACCTTGGGTGCAACAAT 108
DB |||||
QY 61 ATTGTGTCCTCCAAATGTTGTAACAAGATTTGTTACATCTCTCCGGGTACTTTAAGCTGAC 120
DB |||||
QY 109 ATTGTGTCCTCCAAATGTTGTAACAAGATTTGTTACATCTCTCCGGGTACTTTAAGCTGAC 168
DB |||||
QY 121 TAGGACATTCACCAATTTATTTTGGCGTGCATTTGATGCGTGGCAATTTCCCTCCACTTG 180
DB |||||
QY 169 TAGGACATTCACCAATTTATTTTGGCGTGCATTTGATGCGTGGCAATTTCCCTCCACTTG 228
DB |||||
QY 181 GATTAGTCGGGGCGAAAGTCAATCGGTATATTAATCCATCAACTAAGAAATGTCACAGA 240

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Db      229  GATTAGTCGGGGGAAAGTCATCGGTATATTAAATCCATCAACTAAGAATGTCACAGA 288
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Db      289  AATCTAAGTTGTTGAACCTGGCGGAGGCTATCTCGGTAGGGTGTGGCGGTTTACCCC 348
QY      301  ACCCGTGCACCTGCAGGACACCCACCAATCACCAGTCATCCAGAACCTCTACACGAC 360
Db      349  ACCCGTGCACCTGCAGGACACCCACCAATCACCAGTCATCCAGAACCTCTACACGAC 408
QY      361  CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTAGGCGCAT 420
Db      409  CACCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTCCCTAGGCGCAT 468
QY      421  CAATGACCCAGTTGGCTCGATCGAGACGTGGCCACCCCTATCGGGTGGATGCTG 480
Db      469  CAATGACCCACATTTGGCTCGATCGAGACGTGGCCACCCCTATC-GGGTGGATGCGG 527
QY      481  CCCGAGCGTGTATGGACAGTTGTTG--CGTACCTCGATAGTGGCAGCATAAAGTGAAGT 538
Db      528  CCCAAACGATGTATGGACAGTTGTTGGCGGTACCTCGATAGTGACATAGTGAAGT 587
QY      539  CACAAAGCAGAGGGGAGAAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAT 598
Db      588  CACAAAGCAGAGGGGAGAAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAT 647
QY      599  TTATATGAGCAAAATATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 658
Db      648  TTATATGAGCAAAATATTTTGGTACTTTATATATAGGATATGCGGCTTTGGCAC 707
QY      659  TATGATATTAATCGTATATATACCAATATCATACCTTGACTAAATATATATAAATAAT 718
Db      708  TACGGATATTAATCGTATATATACCAATATCATACCTTGACTAAATATATATAAATAAT 767
QY      719  ATTACAAATATGATTTGTTAAACGTTGAGGTGGCAAAATGATTAAGAGCCGCTTAATAT 778
Db      768  ATTACAAATATGATTTGTTAAACGTTGAGGTGGCAAAATGATTAAGAGCCGCTTAATAT 827
QY      779  AATATTTTATGAATATAGACTATAGTTACAAGTGAACCTTTATTTGGTGATACTTTGAC 838
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QY      839  ATATAAACTCTGATCGTACGAGCACTTTCTTAAACTAAATATTAAGAGCAGCTATT 898
Db      888  ATATAAACTCTGATACGTGACGGAATTTCTTAAACTAAATATTAAGAGCAGCTATT 947
QY      899  TTAATATTTTTCGTGGCCAAAGTTTCTTGCACTATCTATGCCATTTTACTTTTAT 958
Db      948  TTCACATTTTCGTGGCCAAAGTCTCTTGCACTATCTATGCCATTTTACTTTTAT 1007
QY      959  CGTTCTAGCCTTTAGGTAGCGGTTTGAACATATAAAATCATATAAATGAAGTAAAAA 1018
Db      1008  CGTTCTAGCCTTTAGGTAGCACGTTTGAACATATAAAATCATATAAATGAAGTAAAAA 1067
QY      1019  TTAG--TTTTTTTTCATATTACTCGPATGGATCTTTGTAGATCAATGTAATATATAC 1075
Db      1068  TTAGTTTTTTTTTTCATATTACTCGPATGGATCTTTGTAGATCAATGTAATATATAC 1127
QY      1076  AATCATCTGATTTTAAATCAATACTATCTGCATGATGGAAAGTGTGATGCTATTC 1135
Db      1128  AAACCATCTGATTTTAAATCAACCACTCTGCCTTAATGGGGAAGTCTAT-GTGATTC 1186
QY      1136  GTGCAAGTGTGTGATTTATTTCTAAGTCTCGATTGGGTGACACACTTTTAGTGCAATAT 1195
Db      1187  GTGCAAGTGTGTGA-TTATCTTAGTCTAGATGGGTGACACACTTTTAGTGCAATAT 1245
QY      1196  CTATTAAGAACCCCTTATTGTATGCAAAAGTCAATAAA--TATTTAATATCATNCTTTA 1253
Db      1246  CTATTAAGAACCCCTTATTGTATGCAAAATATCTATTAAAGAACCCCTTATTCATCTTTA 1305
QY      1254  TTTATTTTACGATCGGACATGATACATTTTACTAATTAATAATTAATTTGAAGGAATTG 1313

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Db      1306  TTTATTTTACGATCGGACATGATATATTTACTAATTAATAAATAAATGGAGAAATTG 1365
QY      1314  ATCGCAAGTCATCAAGCTTATCGTCGATCCATCCCTTAACCTTAGTATGGCTGCTT 1373
Db      1366  ATCGCAAGCCATCAAGCTTATCGTCGATCCATCCCTTAGTATGGCTGCTT 1425
QY      1374  TTAGAGAAACAAGTGCATGTAATAATTTAGTTTCCCTATCTCCCTATATAAATATCTAT 1433
Db      1426  TTAGAGAAACAAGTGCATGTAATAATTTAGTTTCCCTATATAAATATCTCCCTATACCTGT 1485
QY      1434  ATATACCTCTTAAATCAATCAATCAACACAACAATATAAATAGATTTCTTTAAAGA 1493
Db      1486  CTATCCCTCTTAAACCAATCATCTAACAACAACAATATAAATAGATTTCTTTAAAGA 1545
QY      1494  AATTCAGAAATTAATGAGGCAATATAGTCTATGTTGAAGTTGGTTCCTTTC 1546
Db      1546  AATTCAGAAATTAATGAGGCAATATAGTCTATGTTGAAGTTGGTTCCTTTC 1598

RESULT 4
SC81OLP/c      SC81OLP      2659 bp      DNA      linear      PLN 27-OCT-1995
LOCUS      S.commersonii (posML81) gene for osmotin-like protein.
DEFINITION      X72927
ACCESSION      X72927.1      GI:296773
VERSION      osmotin-like protein.
KEYWORDS      Solanum commersonii (Commerson's wild potato)
SOURCE      Solanum commersonii
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE      1
AUTHORS      Zhu, B., Chen, T.H. and Li, P.H.
TITLE      Activation of two osmotin-like protein genes by abiotic stimuli and
      fungal pathogen in transgenic potato plants
JOURNAL      Plant Physiol. 108 (3), 929-937 (1995)
MEDLINE      95357444
PUBMED      7630973
REFERENCE      2 (bases 1 to 2659)
AUTHORS      Zhu, B.
TITLE      Direct Submission
JOURNAL      Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
      Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
COMMENT      Related sequences: M29279 & M21346.
FEATURES      Location/Qualifiers
      source      1..2659
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Query Match      46.2%; Score 715; DB 8; Length 2659;
Best Local Similarity      74.7%; Pred. No. 2.4e-134;
Matches 1170; Conservative      0; Mismatches 180; Indels 217; Gaps 13;

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Db 605 TTTTATGCAAGTATCTATTATAAAGAACCCCTA-TTGATGCAAAATCAAT----- 556
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Db 555 -----AAATAAA 549
Qy 1301 TTGGAGGAAATTGATCGACAAAGTCATCAAGCTTATCGTCGATCCACATTTCCCTTAACGTT 1360
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Qy 1540 TGCTTTC 1546
Db 308 TGCTTTC 302

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RESULT 5
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
SCL130LP
S: commersonii (posML13) gene for osmotin-like protein.
X72928
X72928.1 GI:296771
osmotin-like protein.
Solanum commersonii (Commerson's wild potato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1
Zhu, B., Chen, T.H. and Li, P.H.
Activation of two osmotin-like protein genes by abiotic stimuli and
fungal pathogen in transgenic potato plants
Plant Physiol. 108 (3), 929-937 (1995)
95357444
7630973
2 (bases 1 to 2638)
Zhu, B.
Direct Submission
Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
Related sequences: M29279 & M21346.
Location/Qualifiers
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ORIGIN
Query Match 36.5%; Score 563.6; DB 8; Length 2638;
Best Local Similarity 77.0%; Fred. No. 9.6e-104;
Matches 735; Conservative 0; Mismatches 194; Indels 25; Gaps 3;

QY 1 ATCTTTGTTTGAAGAAATGGAAGAACGTTAGGACACATGAGACCTTGGGTGCAACAAT 60
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DB 1740 AATCTAGTTGTTCACTGTTCCGAGCGTACTCGGCTAGGTTGTTGGGGTTTACCCC 1681
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DB 1680 ACCCGGTGCACTGCAGGACACCAACCAATCACCAGTCAATGAGCAACCTCTACCAAGCAC 1621
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DB 1087 CTTCTAATAAGATTTTTCATTTCTAAAGANTCAAATTCACATGATTAGAAT 1034

RESULT 6
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LOCUS AF093743
DEFINITION Lycopersicon esculentum pathogenesis-related protein osmotin
Precursor (NP24) gene, complete cds.
ACCESSION AF093743
VERSION AF093743.1 GI:3747059
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 1304)
AUTHORS Jia,Y. and Martin,G.B.
TITLE Rapid transcript accumulation of pathogenesis-related genes during
an incompatible interaction in bacterial speck disease-resistant
tomato plants
JOURNAL Plant Mol. Biol. 40 (3), 455-465 (1999)
MEDLINE 99364540
PUBMED 10437829
REFERENCE 2 (bases 1 to 1304)
AUTHORS Martin,G.B. and Jia,Y.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1998) Boyce Thompson Institute, Tower Road,
Ithaca, NY 14853-1801, USA
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ORIGIN
Query Match 35.6%; Score 550.4; DB 8; Length 1304;
Best Local Similarity 78.7%; Fred. No. 4.5e-101;
Matches 711; Conservative 0; Mismatches 181; Indels 12; Gaps 4;

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DB 852 ATTGTTGTCCTCCAAATGTGTGTAAGAATGTTTACATCTCTCCGGGTACTTTAAGCTGAC 793
QY 121 TAGGACATTCACCATTTATATTTCCCGTGCATTTGAATTTGGTGCATTTCCCTCCACTTG 180
DB 792 TAGGACATTCACCATTTATATTTGGCGGTGCAATGAATTTGGTGCATTTTCTCTCCACTAG 733

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QY 181 GATTAGTCGGCGGCAAGTCACTCGTATATTAAATCCATCAACTAAAGAAATGTCACAGA 240
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QY 241 AATCTAGTCTTCTGAACTGGTCCGAGGGTACTCGGCTAGGGTGTTCGGGGTTTACCCC 300
Db 672 AATCTAGTCTTCTGAACTGGTCCGAGGGTACTCGGCTAGGGTGTTCGGGGTTTACCCC 613
QY 301 ACCGGTGCACCTGAGGACACCAACCAATCACCAGTCAATGACGAACTCTACAGCAC 360
Db 612 ATCCGGTACACTGTAAGACTCCACCAATCACCAGTCTGACATGTACCTCTGCTGCAG 553
QY 361 CATCGAAGTTACATCCAGTACAGCCCATATACGTGCAATGAGTCCCTTAGGCGCAT 420
Db 552 CATTAAGATTCGAACCACTAGTACGACCCCATATACGTGCAATGTAGTTCCCTCGAGCAT 493
QY 421 CAATGACCCAGTTTGGCTCGATCGAGAGCTGGCCACCGCTATCGGGTGCATGCTG 480
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QY 481 CCCAGAGCTGTATGGAACAGTTTGGCTACCTCGATAGTGGCAGCAATAAGTGAAGTCA 540
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Db 312 ATATGAGGATACTATTATTTGAAAGCATTATATAGGAGTGTGGCGCTTTTGGCACT 253
QY 560 ATGATATTATCTATATATATCAATATCACTTTGACTATATTAACAAATAATA 719
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QY 899 TTAA 902
Db 22 GTGA 19

RESULT 7
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LOCUS 901 bp mRNA linear PLN 16-MAR-1993
DEFINITION S.commersonii mRNA for osmotin-like protein.
ACCESSION X67121
VERSION X67121.1 GI:21194
KEYWORDS osmotin-like protein.
SOURCE Solanum commersonii (Commerson's wild potato)
ORGANISM Solanum commersonii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 901)
Zhu, B., Chen, I. H. and Li, P. H.
Expression of an ABA-responsive osmotin-like gene during the
induction of freezing tolerance in Solanum commersonii
Plant Mol. Biol. 21 (4), 729-735 (1993)
JOURNAL 93192535
MEDLINE 8448373
PUBMED
REFERENCE 2 (bases 1 to 901)

AUTHORS Zhu, B.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1992) B. Zhu, Dept of Horticulture, AG & Life
Science 4017, Oregon State University, Corvallis OR 97331, USA
FEATURES
Location/Qualifiers
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Best Local Similarity 90.8%; Pred. No. 1.7e-92;
Matches 541; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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Db 66 CAAAGCAAGAGGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTGTTGAAGT 11
RESULT 8

AUTHORS Zhu, B.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1992) B. Zhu, Dept of Horticulture, AG & Life
Science 4017, Oregon State University, Corvallis OR 97331, USA
FEATURES
Location/Qualifiers
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	QY	601	ATATGTGGCAAAATTTTT-----ATTTTTGCTACTTTATATATATAGGGA	640
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	QY	701	TAAATTAAACAAATAATATTACAATATGATTTGGTTGAAGCTTGAGTGGCAAAATGTAT	760
	Dd	1026	TA---GTAAATGGATAAATCTCAAGGATGCTTTAGTAAAGGTGGAGCGGCTAAAAAGTAT	970
	QY	761	AAGAGCGGCTTAAT-AATTAATTTATTTATGAATATAGACTATAGTTACAAGTGAACCTTT	819
	Dd	969	AAGAGCGGCTTAATAAATTAATTTATGAATATAG--ATTTATGAATATAG-----AAGTCAATTT	922
	QY	820	ATTTGGTGATAACTTGGACATATAAACTCTGTATCGTGAC	859
	Dd	921	ATTTGGTGATGATGCTGACCTATAAGCTCTGTAAACGTGAC	882
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	DEFINITION	Sequence 1 from patent US 5801028.		
	ACCESSION	AR037158		
	VERSION	AR037158.1 GI:5955014		
	KEYWORDS	Unknown.		
	SOURCE	Unknown.		
	ORGANISM	Unclassified.		
	REFERENCE	1 (bases 1 to 3033)		
	AUTHORS	Bressan,R. and Hasegawa,P.M.		
	TITLE	Osmotin gene promoter and use thereof		
	JOURNAL	Patent: US 5801028-A 1 01-SEP-1998;		
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	Best Local Similarity	71.1%;	Fred. No. 6.9e-91;	
	Matches 749; Conservative	0; Mismatches 265;	Indels 40; Gaps 5;	
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	Dd	2619 ACTTTGTTTGA AAAAATTTTGA AAAAA ATGTAGG ACCA CAAAGTCTCTTGTGTGCAACAAT	2560	
	QY	61 ATTGTTGCTCTCGAATGTGGTAC AAGGATTTGTTATCCTCTCGG GTACTTTAAGCTGAC	120	
	Dd	2559 ATTGTTGCTCTCGAATGTAGTAC AAGG GTATTATCATCTCTCGG AAACCTTAAGTTTCG	2500	

QY	121	TAGGACATTACCAATTTATATATTTGCCGTGCATTAATGCTGGCATTTCCCTCCACTTG	180
DB	2499	GGGGACATTTCCGCGTTATATTAGCCGTACAATGAATTTGCAATGTCATTTCCCTCCACTAG	2440
QY	181	GATTAGTCGGGGCGGAAAGTCATCGGTATATTAAATCCATCAACTAAAGAAATGTCACAGA	240
DB	2439	GGTTAGTCGGGGCGGAAAGTCATCGGAAATGTTGAATCCATCAACTAAAGAAATGTCACAGA	2380
QY	241	AATCTAAGTTGTTGAACTGTGTCGGAGGGCTACTCGGCTAGGGGTGTTGGCGGTTTACCCC	300
DB	2379	AATCTAAACCACTGAATTTGGTCCAAAGCGTATTGAGCAAGGTTGTTGGTGGTTTACCCQ	2320
QY	301	ACCGGTGCATTCGAGGACACACACAAATCACCAGTCAATGCGACGACCTCTACACGAC	360
DB	2319	ACCGGTGCATCTGAGACTCAACCAAGTCAACCGTTTGGCAGCTACCCCTACGAGAG	2260
QY	361	CATCGAAGTTACATCCAGTACGACCCCATATACGTGCCATCGTAGTGCCTTAGGCGCAT	420
DB	2259	CATTGAAGTTACAATTAGTAGCGGCCCATACACGTGCCATTTTAGTAGCTCGTGGCGCAT	2200
QY	421	CAATGACCCACGTTTGGGCTCGATCGAGACGTGGGCACCGCCTATCGGGTGCATGCTG	480
DB	2199	TGATCACCAAGTTTGGGCTCGATCGAGACCGCGCCACCGCCTATGGGTGTGCAACCG	2140
QY	481	CCCAGACGGTGTATGGACAGTTGTTGCGTACTCGATAGTGGCAGCATAAAGTGAAGTCA	540
DB	2139	CCCAAA CGGTGTACGGACAGTTGTTCGGACCTCGATAGTGGCAGCATTAAGTATAGTCA	2080
QY	541	CAAAAGCAAGAGGGAGGAAAAACAAAAGATCTCAAGTAGTGGCAGCATAAAGTGAAGTCA	600
DB	2079	CCAAGGCAAGGAGGAAGAAAAACAAAAGATCTCAAGTTGCCCATGTTGTTGGACATTT	2020
QY	601	ATATGTGGACAAATATTATTTTGGTACT-----TTATATATAGGGAT	641
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QY	642	ATGCGCGCTTTTGGCCTATCGATTAATTAATCGTATTATATAACAAATATCATACTTTGACT	701
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QY	702	AATTATAAAACAATAATATTACAATATGATTTGGTTAAACGTTGAGGTGGC-AAAATGAT	760
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QY	881	TATTAAAAAGCAGCTATTTTAATTTTTCGTGGCCAAAGTTTCTTCGTACTATTCTAT	940
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QY	941	GCCCATTTTACTTTTATCGTTCTTAGCGTCTTAGGTACGGGTTTGAAACATAAAAAATCAT	1000
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QY	1001	AAAAATTGAAGTAAAAAATAGTTTTTTTTTCATA	1034
DB	1619	AAAAATAAACTCAACCAATAATATTCGTCAAAA	1586

RESULT 10	S40046	3033 bp	DNA	linear	PLN 17-APR-2000
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LOCUS					
DEFINITION	S40046	3033 nt	acid-activated	Nicotiana glauca	L. tobacco, leaf,
ACCESSION	S40046				
VERSION	S40046.1	GI:251138			

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KEYWORDS
SOURCE
ORGANISM
Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 3033)
Nelson,D.E., Raghothama,K.G., Singh,N.K., Hasegawa,P.M. and
Bressan,R.A.
Analysis of structure and transcriptional activation of an osmotin
gene
JOURNAL
Plant Mol. Biol. 19 (4), 577-588 (1992)
MEDLINE
92329718
PUBMED
1385735
REMARK
GenBank staff at the National Library of Medicine created this
entry [NCBI Gibbs 108425] from the original journal article.
This sequence comes from Fig. 1A.
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Best Local Similarity	71.1%	Pred. No. 6.9e-51;		
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				Gaps 5;

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Db	2559	ATTGTTGCTCCT	2500
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Db	2499	GGGGACATT	2440
Qy	181	GATTAGTCGGG	240
Db	2439	GTTTGTTCGGG	2380
Qy	241	AATCTAAGTTG	300
Db	2379	AATCTAACC	2320
Qy	301	ACCCGTTGCA	360
Db	2319	ACCCGTTGCA	2260
Qy	361	CATCGAAGTT	420
Db	2259	CATTGAAGTT	2200
Qy	421	CAATGACCC	480

Db 2199 TGATCACCAGATTGGCTCGATCGAGACGGCGCCACCGCTATGGGTGTCGACGCCG 2140
 QY 481 CCCAGACGGTGTATGGACAGTTGTCGGTACCTCGATAGTGGCAGCATAGTGAAGTCA 540
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 QY 541 CAAAGCAAGAGGAGGAGAAACAAAGAGATCTCAAGTAGCCCATGTTTGTGAATTT 600
 Db 2079 CCAAGGCAAGGAGGAGAAACAAAGAGATCTCAAGTTGCCCATGTTGTTGGACATTT 2020
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 Db 1619 AAAATAAAACTCAAAACAATAATATTCGTCAAAA 1586

RESULT 11
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 DEFINITION N.tabacum ap24 gene.
 ACCESSION X65701
 VERSION X65701.1 GI:119782
 KEYWORDS osmotin.
 SOURCE Nicotiana tabacum (common tobacco)
 ORGANISM Nicotiana tabacum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1
 AUTHORS Melchers,L.S., Sela-Buurlage,M.B., Vloemans,S.A., Woloshuk,C.P., Van Roekel,J.S., Pen,J., van den Elzen,P.J. and Cornelissen,B.J.
 TITLE Extracellular targeting of the vacuolar tobacco proteins AP24, chitinase and beta-1,3-glucanase in transgenic plants
 JOURNAL Plant Mol. Biol. 21 (4), 583-593 (1993)
 MEDLINE 93192519
 PUBMED 8448358
 REFERENCE 2 (bases 1 to 1549)
 AUTHORS Melchers,L.S.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-1992) L.S. Melchers, Mogen International NV, Einsteinweg 97, 2333 CB Leiden, THE NETHERLANDS
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Db 424 TTTTAAACAGTGTGGTGTGGTATATAGTGACAAATTTGTAGTGGTTTATATAGGGA 365
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LOCUS S.commersonii (pA81) mRNA for osmotin-like protein.
DEFINITION X72926.1 GI:296775
ACCESSION osmotin-like protein.
VERSION Solanum commersonii (Commerson's wild potato)
KEYWORDS Solanum commersonii
SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ORGANISM Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 977)
AUTHORS Zhu, B., Chen, T.H. and Li, P.H.
TITLE Expression of three osmotin-like protein genes in response to
osmotic stress and fungal infection in potato
JOURNAL Plant Mol. Biol. 28 (1), 17-26 (1995)
MEDLINE 9306785
PUBMED 7787181
REFERENCE 2 (bases 1 to 977)
AUTHORS Zhu, B.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1993) B. Zhu, Oregon State University, Dept of
Horticulture, AG. & Life Science 4017, Corvallis, OR 97331, USA
COMMENT Related sequences: M29279 & M21346.
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Best Local Similarity 87.8%; Pred. No. 6.9e-88;
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QY 121 TAGGACATTCACCATTTATATTGCGGTGCATTAATTCGTTGGGATTTCCCTCCACTTG 180
Db 500 GAGGACATTCACCATTTATATTGGCGGTGCATTAATTCGTTGGGATTTCCCGACACTAG 441
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Db 440 GTTTGTTGTCGGGCGAAAGTCATTCGAATATTCGAATCCGTCAACTAAAGAAATATCCG 381
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Db 380 AATCTAGGTGCTAAACTGATCCAGGCGATATTCAGCAAGGTGTTTGGGCGCTTACCCC 321
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Db 20 ATTTATATGAGGACAAATTA 1
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LOCUS Lycopersicon esculentum PR-5x (PR-5) mRNA, complete cds.
DEFINITION AY093595
ACCESSION AY093595
VERSION AY093595.1 GI:20750096
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SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
REFERENCE 1 (bases 1 to 917)
AUTHORS Rep.M., Dekker,H.L., Vossen,J.H., De Boer,A.D., Houterman,P.M.,
Speijer,D., Back,J.W., De Koster,C.G. and Cornelissen,B.J.C.
TITLE Mass Spectrometric Identification of Isoforms of PR Proteins in
Xylem Sap of Fungus-Infected Tomato
JOURNAL Plant Physiol. 130 (2), 904-917 (2002)
MEDLINE 22264016
PUBMED 12376655

REFERENCE 2 (bases 1 to 917)
 AUTHORS Rep.M., Dekker H., Vossen, J.H., de Boer, A., Houterman, P.,
 Speijer, D., Back, J.-W. and Cornelissen, B.J.C.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-2002) Plant Pathology, University of Amsterdam,
 Kruislaan 318, Amsterdam 1098SM, Netherlands
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Jami, S.K. and Kirti, P.B.
 TITLE PCR-based cloning of an osmotin-like protein gene from Solanum
 nigrum
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 729)
 AUTHORS Jami, S.K. and Kirti, P.B.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2002) Department of Plant Sciences, University of
 Hyderabad, Gachibowli, Hyderabad, A.P 500046, India
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ACCESSION     AF450276
VERSION       AF450276.1   GI:19401630
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REFERENCE     1 (bases 1 to 744)
AUTHORS      Campos,M.A., Ribeiro,S.G., Rigden,D.J., Monte,D.C. and Grossi de
               Sa,M.F.
TITLE         Pathogenesis related-like genes of Solanum nigrum: cloning and
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JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 744)
AUTHORS      Campos,M.A., Ribeiro,S.G., Monte,D.C. and Grossi de Sa,M.F.
TITLE         Direct Submission
JOURNAL       Submitted (21-NOV-2001) PBI, Embrapa Genetic Resources and
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Query Match 31.0%; Score 480; DB 8; Length 744;
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Matches 519; Conservative 1; Mismatches 66; Indels 0; Gaps 0;
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